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Scientific and Technical Information Center

SEARCH REQUEST FORM

3-
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OCT 20 2006

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10/19/06
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 09/544,776
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Novel Cell Stress Protein
Inventors (please provide full names): Dong Wei et al.

Earliest Priority Date: 4-10-00

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search in Seq ID No 2
per phone call
Size limit to 25 NTS. 8-30
Please include Interference d to
base.

Thanks.

AA 373

p2n

8-30

150 summaries 50 results 8-50

BEST AVAILABLE COPY

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ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560A24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ALIGNMENTS

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

1.97e+05

53.00

88.9%

Length:

Matches:

Conservative:

29

8

0

Best Local Similarity: 88.9% Mismatches: 1
 Query Match: 2.8% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ764536 (1-29)

QY 140 ProAlaAArgProProProProPro 148
 LOCUS |||||
 Db 28 CCCCCCGCCCCCCCCCCCCCCCCCCCC 2

RESULT 2

BQ592681/c
 LOCUS |||||
 DEFINITION S01324-024-028-B02-T7 MP1Z-ADIS-024-developing root Beta vulgaris
 CNA clone 024-028-B02 3-PRIME, mRNA sequence.

ACCESSION BQ592681
 VERSION BQ592681
 KEYWORDS EST.

ORGANISM

Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

PUBMED 12472698

COMMENT

Contact: Weissshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 30 Std Error: 0.00

Plate: 28 row: B column: 02

Seq primer: T7; GTAATACGACTACTATAGGC.

FEATURES

source

1. .30
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 /clone="024-028-B02"
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 /clone_lib="MP1Z-ADIS-024-developing root"
 /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfelderleber Saatzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x BQ592681 (1-30)

QY 139 ProProAlaAArgProProProProPro 148
 LOCUS |||||
 Db 30 CCCCCCGCCCCCCCCCCCCCCCCCCCC 1

RESULT 3

CX002837

LOCUS |||||

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;

Canis.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org.

Location/Qualifiers

1. .30

/organism="Canis familiaris"

/mol_type="mRNA"

/db_xref="taxon:9615"

/sex="Unknown"

/tissue_type="Cardiac muscle"

/dev_stage="3 month old normal canine"

/lab_host="XL10 Gold"

/clone_lib="Left Cardiac Ventricle (DOGEST7)"

/notes="Organ: Heart; Vector: pBluescript II SK; Site 1:

EcoRI; Site 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,

Pathology and Medical Genetics, School of Veterinary

Medicine, University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 8 Gaps: 0

US-09-544-776-2 (1-373) x CX002837 (1-30)

QY 139 ProProAlaAArgProProProProPro 148
 LOCUS |||||

Db 1 CCCCCCGCCCCCCCCCCCCCCCCCCCC 30

RESULT 4

DR073122

LOCUS |||||

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ginkgo biloba (maidenhair tree)

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DR073122 ik86f07.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 sequence.

DR073122 DR073122.1 GI:67050973

EST.

Ginkgo biloba (maidenhair tree)

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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REFERENCE
AUTHORS      Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 30)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NVBG)
JOURNAL      Unpublished (2005)
COMMENT      Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES
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1..30
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Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."
ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
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US-09-544-776-2 (1-373) x DR073122 (1-30)
QY 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCG 30
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LOCUS 1M0040C18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0040C18 F, genomic survey sequence.
ACCESSION AZ320274
VERSION AZ320274.1 GI:10371888
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x AZ320274 (1-30)
QY 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCG 30
RESULT 6
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LOCUS 1M0045N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0045N05 F, genomic survey sequence.
ACCESSION AZ323580
VERSION AZ323580.1 GI:10378439
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT

```

```

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: N column: 05
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Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ232580 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
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Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 7
AZ389258
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: K column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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1. 30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0149K12"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ389258 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
|||||
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 8
AZ390605/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

30 bp DNA linear GSS 03-OCT-2000
IM0152P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0152P01 F, genomic survey sequence.
AZ390605
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: P column: 01
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0152P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ390605 (1-30)

QY 139 ProProAlaArgProProProProPro 148
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DB 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 9
AZ412491/c
LOCUS
DEFINITION 30 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0186A03 F, genomic survey sequence.
ACCESSION AZ412491
VERSION AZ412491.1 GI:10536504

```

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KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS      1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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plasmid inserts
JOURNAL
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Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ412491 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
DB 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 10

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Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ468615 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
 DB 1 CCCCCCCCCCTCCCCCCCCCCCCCCCCCCCCC 30

RESULT 12

AZ487848 30 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0317H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0317H13 R, genomic survey sequence.

ACCESSION AZ487848
 VERSION AZ487848.1 GI:10655974

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 30)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0317 row: H column: 13

Seq primer: CACACGAGAACGATGAC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

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/clone="UUGC1M0317H13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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electrophoresis. Vector DNA was prepared from a derivative

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inducible derivative of plasmid R1. The vector was ligated

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purified. The sheared, adaptored mouse DNA was annealed to

and selected for ampicillin resistance."

Alignment Scores: 2.06e+05 Length: 30
 Pred. No.: 53.00 Matches: 8
 Score: 80.0% Conservative: 0
 Percent Similarity: 80.0% Mismatches: 2
 Best Local Similarity: 80.0% Indels: 0
 Query Match: 2.8% Gaps: 0
 DB: 11

US-09-544-776-2 (1-373) x AZ487848 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
 DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 13

AZ490365/c

LOCUS 1M0323J14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0323J14 F, genomic survey sequence.

ACCESSION AZ490365

VERSION AZ490365.1 GI:10661022

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 30)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0323 row: J column: 14

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1. .30

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/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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ligated to the blunt ends in high molar excess. The

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electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ650045 (1-30)

QY 139 ProProAlaArgProProProProProPro 148

DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 16

AZ764531/c

LOCUS AZ764531 30 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0560M15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560M15 R, genomic survey sequence.

ACCESSION AZ764531

VERSION AZ764531.1 GI:12879589

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: M column: 15

Seq primer: CACACGAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ764531 (1-30)

QY 139 ProProAlaArgProProProProProPro 148

DB 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 17

AZ788303

LOCUS AZ788303

DEFINITION 2M0035K15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035K15 F, genomic survey sequence.

ACCESSION AZ788303

VERSION AZ788303.1 GI:12927967

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: K column: 15

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

FEATURES

source

1. 30

/organism="Mus musculus"

/mol_type="genomic DNA"

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ807237 (1-30)

QY 139 ProProAlaArgProProProProPro 148

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 19

AZ824951

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

84112, USA

20 S. 2030 E., SLC, UT

20 S. 2030 E., SLC, UT

20 S. 2030 E., SLC, UT

20 S. 2030 E., SLC, UT

20 S. 2030 E., SLC, UT

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20 S. 2030 E., SLC, UT

20 S. 2030 E., SLC, UT

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: E column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2,06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x AZ824951 (1-30)
QY 139 ProProAlaArgProProProProPro 148
DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30
RESULT 20
AZ845409/c 30 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0145N10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0145N10 F, genomic survey sequence.
ACCESSION AZ845409
VERSION AZ845409.1 GI:13015317
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: E column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099E19"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2,06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x AZ824951 (1-30)
QY 139 ProProAlaArgProProProProPro 148
DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30
RESULT 20
AZ845409/c 30 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0145N10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0145N10 F, genomic survey sequence.
ACCESSION AZ845409
VERSION AZ845409.1 GI:13015317
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: N column: 10
Seq primer: CGTTGTAACAGCGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0145N10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 2,06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x AZ845409 (1-30)
QY 139 ProProAlaArgProProProProPro 148
DB 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1
RESULT 21
AZ861881 30 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0168J17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0168J17 R, genomic survey sequence.
ACCESSION AZ861881
VERSION AZ861881.1 GI:13058644
KEYWORDS GSS.


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Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 23
LOCUS DU833421 30 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS012B18f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS012B18, genomic survey
sequence.
ACCESSION DU833421
VERSION DU833421.1 GI:83870017
KEYWORDS GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 30)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
END sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
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225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa sep. pekinensis Sau3AI BAC clone
KBrS015C14
Seq primer: T7
Class: BAC ends.
LOCATION/Qualifiers
source 1..30
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS015C14"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1, Site 1: Sau3AI; Brassica rapa
asp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

FEATURES
Location/Qualifiers
source 1..30
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1, Site 1: Sau3AI; Brassica rapa
asp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0
US-09-544-776-2 (1-373) x DU834752 (1-30)
Qy 139 ProProAlaArgProProProProPro 148
Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 25
LOCUS DU835509 30 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016N01F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016N01, genomic survey
sequence.
ACCESSION DU835509
VERSION DU835509.1 GI:83872105
KEYWORDS GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 30)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
END sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team

```

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225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS016P03
Seq primer: T7
Class: BAC ends.

FEATURES

source
1. .30
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
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/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016P03"
/lab_host="E. coli DH10B"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

ORIGIN

Alignment Scores:

Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DU835509 (1-30)

Qy 139 ProProAlaArgProProProProPro 148

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCA 30

RESULT 26

DU835563

LOCUS DU835563 30 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016P03F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016P03, genomic survey sequence.

ACCESSION

DU835563.1 GI:83872159

VERSION

GSS.

KEYWORDS

Brassica rapa subsp. pekinensis

SOURCE

Brassica rapa subsp. pekinensis

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 30)

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

TITLE

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL

Unpublished (2005)

COMMENT

Contact: Beom-Seok Park

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225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBrS016P03

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .30

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

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/db_xref="taxon:51351"
/clone="KBrS016P03"
/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"

/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

ORIGIN

Alignment Scores:

Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DU835563 (1-30)

Qy 139 ProProAlaArgProProProProPro 148

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 27

DX046348

LOCUS

DX046348 30 bp DNA linear GSS 10-JAN-2006

DEFINITION

KBrB047P23R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047P23, genomic survey sequence.

ACCESSION

DX046348.1 GI:84740645

VERSION

GSS.

KEYWORDS

Brassica rapa subsp. pekinensis

SOURCE

Brassica rapa subsp. pekinensis

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 30)

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

TITLE

End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL

Unpublished (2005)

COMMENT

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB047P23

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

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/clone="KBrB047P23"

/lab_host="E. coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

ORIGIN

Alignment Scores:

Pred. No.: 2.06e+05 Length: 30

Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DX046348 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

Db
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 28
DX079739/c
LOCUS
DEFINITION
KBrB092A24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB092A24, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone

TITLE
JOURNAL
COMMENT
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrB092A24
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..30
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/lab_host="E.coli DH10B"
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/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DX079739 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

Db
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 28
DX079739/c
LOCUS
DEFINITION
KBrB092A24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB092A24, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone

TITLE
JOURNAL
COMMENT
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrB092A24
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
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/organism="Brassica rapa subsp. pekinensis"
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/sub_species="pekinensis"
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/clone="KBrB092A24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DX079739 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

Db
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 29
DX079739/c
LOCUS
DEFINITION
KBrB092A24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB092A24, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone

TITLE
JOURNAL
COMMENT
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrB092A24
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..30
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/clone="KBrB092A24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DX079739 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

Db
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 29
DX079739/c
LOCUS
DEFINITION
KBrB092A24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB092A24, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone

TITLE
JOURNAL
COMMENT
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrB092A24
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
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/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
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/clone="KBrB092A24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

ORIGIN
Alignment Scores:
Pred. No.: 2.06e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DX079739 (1-30)

QY 139 ProProAlaArgProProProProPro 148
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

Db
|||||
1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 29
DX079739/c
LOCUS
DEFINITION
KBrB092A24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB092A24, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H.

AUTHORS	Viehoever, P., Holtgraewe, D. and Weisshaar, B.
TITLE	BAC end sequences of <i>Brassica rapa</i>
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 30)
AUTHORS	Li, Y. and Weisshaar, B.
TITLE	Direct Submission
JOURNAL	Submitted (09-AUG-2005) Weisshaar B., Bielefeld University, Institute for Genome Research, Universitaetsstrasse 25, D-33594 Bielefeld, Germany
COMMENT	Contact: Bernd Weisshaar Bielefeld University, Institute for Genome Research Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email: bernd.weisshaar@uni-bielefeld.de BAC end sequences of <i>Brassica rapa</i> BAC clone KBrH19J10; generated as contribution to the 'Multinational <i>Brassica rapa</i> Sequencing Project', Seq primer: sp6B ATTTCAGTCACTATAG Class: BAC ends.

```

ORIGIN
Alignment Scores:
Pred. No.:      2.06e+05      Length:      30
Score:          53.00        Matches:     8
Percent Similarity: 80.0%    Conservative: 0
Best Local Similarity: 80.0% Mismatches:   2
Query Match:     2.8%       Indels:       0
DB:              14         Gaps:       0

US-09-544-776-2 (1-373) x CT012008 (1-30)

Qy      139 ProProLaArgProProProProPro 148
      |||||
Db      30 CCCCCCCCCCCCCCCCCCCCCCCCCC 1
      |||||

RESULT 31
DR41F20T/c
LOCUS      DR41F20T      30 bp      DNA      linear      GSS 22-NOV-2002
DEFINITION Dario reio genomic clone DKEX-41F20, genomic survey sequence.
```

```

/tissue_type="Testis"
/notes="vector pindigobAC-536"

ORIGIN
Alignment Scores:
Pred. No.:      2.06e+05      Length:      30
Score:          53.00      Matches:      8
Percent Similarity: 80.0%      Conservative: 0
Best Local Similarity: 80.0%      Mismatches: 2
Query Match:    2.8%      Indels:      0
DB:            14      Gaps:        0

US-09-544-776-2 (1-373) x DR41F20T (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 32
TA28A09P
LOCUS      30 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 28a09, forward sequence,
           genomic survey sequence.
ACCESSION  AL454157
VERSION    AL454157.1 GI:11852635
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
           Trypanosoma brucei
           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
           Trypanosoma.
REFERENCE  1 (bases 1 to 30)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
           Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
           Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE     Direct Submission
JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
           project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
           Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
           nh@sanger.ac.uk
COMMENT   Constructed at the Institute for Genomic Research (TIGR),
           Rockville, MD. Genomic DNA isolated from a cloned population of
           Trypanosoma brucei (TREU27/4 GUTat 10.1) was mechanically sheared
           to give a tight size distribution (
           4 kb). The v + i method used for the library construction is
           described in detail in Smith, H. and Venter, J.C. (Making small
           insert libraries for whole genome shotgun sequencing projects. In
           Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
           Barrell, Oxford University Press, 1999).
           Email: melsayed@tigr.org
           Details of T. brucei sequencing at the Sanger Centre are available
           at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES             source
           Location/Qualifiers
           1..30
           /organism="Trypanosoma brucei"
           /mol_type="genomic DNA"
           /strain="TREU27"
           /db_xref="taxon:5691"
           /clone="28a09"

ORIGIN
Alignment Scores:
Pred. No.:      2.06e+05      Length:      30
Score:          53.00      Matches:      8
Percent Similarity: 80.0%      Conservative: 0
Best Local Similarity: 80.0%      Mismatches: 2
Query Match:    2.8%      Indels:      0
DB:            14      Gaps:        0

US-09-544-776-2 (1-373) x TA28A09P (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 1  CCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

```

```

RESULT 33
AZ864315/c
LOCUS
DEFINITION
  2M0173P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0173P16 R, genomic survey sequence.
ACCESSION
  AZ864315
VERSION
  AZ864315.1 GI:13063493
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 30)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0173 row: P column: 16
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 30.
FEATURES
  source
    1..30
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0173P16"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.: 2.39e+05 Length: 30
Score: 52.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

```

```

US-09-544-776-2 (1-373) x AZ864315 (1-30)
QY 139 ProProAlaArgProProProProProPro 148
Db 30 CCCCCCACCACCCCCCCCCCCCCCCCCCCCCC 1
RESULT 34
AZ641783/c
LOCUS
DEFINITION
  AZ641783 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0504E06 R, genomic survey sequence.
ACCESSION
  AZ641783
VERSION
  AZ641783.1 GI:11766097
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 29)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0504 row: E column: 06
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 29.
FEATURES
  source
    1..29
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0504E06"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
ORIGIN
Alignment Scores:

```


Pred. No.: 2.66e+05 Length: 29
 Score: 51.00 Matches: 8
 Percent Similarity: 88.9% Conservative: 0
 Best Local Similarity: 88.9% Mismatches: 1
 Query Match: 2.7% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ641783 (1-29)

QY 140 ProAlaAgtProProProProPro 148
 Db 28 CCGGCCCCCCCCCCCCCCCCCCCCCCCC

RESULT 35
 AZ8333458/c

LOCUS 30 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0115L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0115L02 R, genomic survey sequence.

ACCESSION AZ8333458
 VERSION AZ8333458.1 GI:13003366
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse).

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduwn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0115 row: 1 column: 02
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 30.
 Location/Qualifiers
 1..30

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0115L02"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to

ORIGIN

Alignment Scores:

Pred. No.: 3.21e+05 Length: 30
 Score: 50.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.6% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ8333458 (1-30)

QY 143 ProProProProProAlaSer 150

Db 28 CCCCCCCCCCCCCCCCCCCCCCCCC

RESULT 36

BQ593191/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 28 Std Error: 0.00

Plate: 27 row: M column: 17

Seq primer: SP6; CATACGATTGAGTGACACTATAG.

Location/Qualifiers

1..28

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:193668"

/db_xref="taxon:161934"

/clone="024-027-M17"

/tissue_type="developing root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-developing root"

/note="Vector: PCWVSP0R6; Site 1: Sali; Site 2: NotI;

CDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Pred. No.: 3.21e+05 Length: 30
 Score: 50.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.6% Indels: 0
 DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ8333458 (1-30)

QY 143 ProProProProProAlaSer 150

Db 28 CCCCCCCCCCCCCCCCCCCCCCCCC

RESULT 36

BQ593191/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 28 Std Error: 0.00

Plate: 27 row: M column: 17

Seq primer: SP6; CATACGATTGAGTGACACTATAG.

Location/Qualifiers

1..28

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:193668"

/db_xref="taxon:161934"

/clone="024-027-M17"

/tissue_type="developing root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-developing root"

/note="Vector: PCWVSP0R6; Site 1: Sali; Site 2: NotI;

CDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

Alignment Scores:
Pred. No.: 3.98e+05 Length: 28
Score: 48.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.5% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x BQ593191 (1-28)

Qy 139 ProAlaArgProProProProPro 147
Db 28 CCCCCCAATCCCCCCCCCCCCCCCC 2

RESULT 37
CJ054334/c 29 bp mRNA linear EST 24-OCT-2005
LOCUS CJ054334 RIKEN full-length enriched mouse cDNA library, C57BL/6J
DEFINITION diencephalon male adult Mus musculus cDNA clone 9330154L15 5', mRNA
sequence.
ACCESSION CJ054334
VERSION CJ054334
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 29)
TITLE The PANTOM Consortium and RIKEN Genome Exploration Research Group
JOURNAL and Genome Science Group (Genome Network Project Core Group).
PUBMED The transcriptional landscape of the mammalian genome
16141072 Science 309 (5740), 1559-1563 (2005)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suihoro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in RIKEN
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/.
FEATURES
source
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9330154L15"
/sex="male"
/tissue_type="diencephalon"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched mouse cDNA library,
C57BL/6J diencephalon male adult"

ORIGIN
Alignment Scores:
Pred. No.: 4.16e+05 Length: 29
Score: 48.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.5% Indels: 0
DB: 5 Gaps: 0

US-09-544-776-2 (1-373) x CJ054334 (1-29)

```

```

Qy 140 ProAlaArgProProProProPro 148
Db 27 CCCCCNNCCCCCCCCCCCCCCCCCCC 1

RESULT 38
CJ054334/c 29 bp DNA linear GSS 22-DEC-2005
LOCUS KRS010N10F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS010N10, genomic survey
sequence.
ACCESSION DU832768
VERSION DU832768.1 GI:83869364
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eustosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 29)
TITLE Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
AUTHORS Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
JOURNAL End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
COMMENT Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.wo.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS010N10
Seq primer: T7
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..29
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS010N10"
/lib_hosts="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

ORIGIN
Alignment Scores:
Pred. No.: 4.16e+05 Length: 29
Score: 48.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.5% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x DU832768 (1-29)

Qy 139 ProProAlaArgProProProProPro 147
Db 28 CCCCCCCCCCACCACCCCCCCCCCCCC 2

RESULT 39
CJ054334/c 30 bp DNA linear GSS 21-FEB-2001
LOCUS AZ875577
DEFINITION 2M0190G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0190G06 F, genomic survey sequence.
ACCESSION AZ875577
VERSION AZ875577.1 GI:13085557
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: G column: 06
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
FEATURES
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0190G06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.: 4,33e+05 Length: 30
Score: 48.00 Matches: 7
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 77.8% Mismatches: 1
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ875577 (1-30)

QY 140 ProAlaArgProProProProPro 148
||||:|||||
DB 1 CCTCTCCCCCCCCCCCCCCCCCCCC 27

RESULT 40
AZ345794/c
LOCUS
Mus musculus house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.: 3,25e+05 Length: 21
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ345794 (1-21)

QY 142 ArgProProProProProPro 148

```

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Db      21  CGCCCCCCCCCCCCCCCCCCCC 1

RESULT 41
A2764532      23 bp      DNA      linear      GSS 16-FEB-2001
LOCUS      1M0560M18 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0560M18 R, genomic survey sequence.
ACCESSION      A2764532
VERSION      A2764532.1 GI:12879591
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 23)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weisse,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0560 row: M column: 18
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
            Location/Qualifiers
                1..23
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0560M18"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
Alignment Scores:      3.63e+05      Length:      23+
Pred. No.:      47.00      Matches:      7
Score:      100.0%      Conservative:      0
Percent Similarity:      100.0%
Best Local Similarity:      100.0%

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Query Match:      2.5%      Indels:      0
DB:      11      Gaps:      0

US-09-544-776-2 (1-373) x AZ764532 (1-23)

Qy      142 ArgProProProProProPro 148
Db      1  CGCCCCCCCCCCCCCCCCCCCC 21

RESULT 42
A2656029      24 bp      DNA      linear      GSS 14-DEC-2000
LOCUS      1M0531O18f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0531O18 F, genomic survey sequence.
ACCESSION      A2656029
VERSION      A2656029.1 GI:11793175
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weisse,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0531 row: O column: 18
            Seq primer: CGTTGTAAACAGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
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                1..24
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0531O18"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN

```

```

Alignment Scores:
Pred. No.:      3.83e+05      Length:      24
Score:          47.00         Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match:     2.5%          Indels:      0
DB:              11           Gaps:       0

US-09-544-776-2 (1-373) x AZ656029 (1-24)

Qy  142 ArgProProProProPro 148
Db  2 CGCCCCCCCCCCCCCCCC 22

RESULT 43
LOCUS      CF322698      22 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION HDN--01-N01.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
            clone HDN--01-N01, mRNA sequence.
ACCESSION  CF322698
VERSION     CF322698.1 GI:33793628
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            1..22
                Location/Qualifiers
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                /mol_type="mRNA"
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                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli SOLR"
                /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                phage cDNA library II (HDN)"
                /notes="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
                XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
                5' end with EcoRI and 3' end with XhoI site. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

ORIGIN
Alignment Scores:
Pred. No.:      4e+05      Length:      22
Score:          46.00         Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match:     2.4%          Indels:      0
DB:              5           Gaps:       0

US-09-544-776-2 (1-373) x CF322698 (1-22)

Qy  143 ProProProProProPro 149
Db  21 CCCCCCCCCCCCCCCCC 11

RESULT 44
LOCUS      AZ953424      22 bp      DNA      linear      GSS 27-APR-2001
DEFINITION 2M0218J08R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0218J08 R, genomic survey sequence.
ACCESSION  AZ953424
VERSION     AZ953424.1 GI:13824651
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0218 row: J column: 08
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.

FEATURES
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            1..22
                Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0218J08"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC2M library"
                /note="Vector: FWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (female) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (GI:4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.:      4e+05      Length:      22
Score:          46.00         Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match:     2.4%          Indels:      0
DB:              11           Gaps:       0

```

US-09-544-776-2 (1-373) x AZ5833424 (1-22)

QY 143 ProProProProProProA 149
 DB 2 CCCCCCCCCCCCCCCCCGCC 22

RESULT 45

AZ583357/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0378C24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-544-776-2 (1-373) x AZ583357 (1-25)

QY 143 ProProProProProProA 149

DB 23 CCCCCCCCCCCCCCCCCGCC 3

RESULT 46

AZ861766

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0168K19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-09-544-776-2 (1-373) x AZ583357 (1-25)

QY 143 ProProProProProProA 149

DB 23 CCCCCCCCCCCCCCCCCGCC 3

RESULT 46

AZ861766

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0168K19"

/sex="Male"

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/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.67e+05 Length: 25
Score: 46.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ861766 (1-25)

QY 143 ProProProProProPro14 149

Db 1 CCCCCCCCCCCCCCCCCCCCCC 21

RESULT 47

CF337419

LOCUS 26 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--07-N14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF337419

VERSION CF337419.1 GI:33823238

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..26 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-N14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 4.9e+05 Length: 26
Score: 46.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 5 Gaps: 0

US-09-544-776-2 (1-373) x CF337419 (1-26)

QY 139 ProProAlaArgProProPro14 146

Db 2 CCCCCCCCCCCCCCCCCCCCCC 25

RESULT 48

AZ604431

LOCUS 26 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0425114F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0425114 F, genomic survey sequence.

ACCESSION AZ604431

VERSION AZ604431.1 GI:11726621

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0425 row: 1 column: 14

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1..26 Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0425114"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.9e+05 Length: 26
Score: 46.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ604431 (1-26)

QY 143 ProProProProProProAla 149
DB 5 CCCCCCCCCCCCCCCCCCGGCC 25

RESULT 49

AZ660002 26 bp DNA linear GSS 14-DEC-2000
LOCUS IM0537L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0537L18 R, genomic survey sequence.

ACCESSION AZ660002
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 row: L column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0537L18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1/4732114|GB|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 4.9e+05 Length: 26
Score: 46.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x AZ660002 (1-26)

QY 143 ProProProProProProAla 149

DB 5 CCCCCCCCCCCCCCCCCCGGCC 25

RESULT 50

AM042721/c

LOCUS

DEFINITION

AM042721 Schistosoma mansoni lung schistosomulum Schistosoma

AM042721

ACCESSION

AM042721

VERSION

AM042721.1

KEYWORDS

EST.

SOURCE

Schistosoma mansoni

ORGANISM

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigoida; Schistosomatoidea; Schistosomidae; Schistosoma.

REFERENCE

1 (bases 1 to 27)

AUTHORS

Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

JOURNAL

COMMENT

Contact: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

Location/Qualifiers

1. .27

FEATURES

source

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="SmlC53e01.q1k"

/dev_stage="lung schistosomulum"

/clone_lib="Schistosoma mansoni lung schistosomulum"

/note="country: Puerto Rico"

ORIGIN

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Score: 46.00 Matches: 7
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Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 1 Gaps: 0

US-09-544-776-2 (1-373) x AM042721 (1-27)

QY 139 ProProAlaArgProProProPro 147

DB 27 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

Search completed: October 21, 2006, 06:01:45

Job time : 5891 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 21, 2006, 04:10:17 ; Search time 7140 Seconds

(without alignments)
5011.006 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLDQSLVSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 373

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1789548

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spo3/US09544776/runat_20102006_110004_23094/app_query.fasta_1
-DB=GenEmbl -QFMT=fastcap -SUFFIX=p2n.szlm8-30.rge -MINMATCH=0.1 -DOOPCL=0
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=150 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=8 -MAXLEN=30
-HOST=abes03h -USER=US09544776 @CGN 1 1 5548 @runat_20102006_110004_23094
-NCPU=6 -ICPU=3 -NO MAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_beg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	53	2.8	30	2	A62996 Sequence 8
3	53	2.8	30	2	AR179065 Sequence

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CS130457	Sequence	30	2	CS130457	Sequence
CS172228	Sequence	30	2	CS172228	Sequence
AR202764	Sequence	30	2	AR202764	Sequence
I84401	Sequence	30	2	I84401	Sequence
I84402	Sequence	30	2	I84402	Sequence
I84403	Sequence	30	2	I84403	Sequence
AX104904	Sequence	30	2	AX104904	Sequence
AX477343	Sequence	30	2	AX477343	Sequence
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I06458	Sequence	28	2	I06458	Sequence
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AR534108	Sequence	30	2	AR534108	Sequence
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AR120087	Sequence	28	2	AR120087	Sequence
E44025	Novel human	28	2	E44025	Novel human
I41109	Sequence	28	2	I41109	Sequence
I41110	Sequence	28	2	I41110	Sequence
I41113	Sequence	28	2	I41113	Sequence
I41118	Sequence	28	2	I41118	Sequence
I41119	Sequence	28	2	I41119	Sequence
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AX104578	Sequence	28	2	AX104578	Sequence
AX355143	Sequence	28	2	AX355143	Sequence
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CS079965	Sequence	29	2	CS079965	Sequence
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AR173054	Sequence	30	2	AR173054	Sequence
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AR242044	Sequence	30	2	AR242044	Sequence
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84 45 2.4 30 2 AR182063 Sequence
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91 44 2.3 30 2 AR138452 Sequence
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DD200037 Method an
DD200037 Method an
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AR182063 Sequence
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AR428114 Sequence
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BD252102 Antiprol
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AX547420 Sequence
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BD241888 Antisense
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AR607448 Sequence
AR608716 Sequence

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ALIGNMENTS

RESULT 1
A62990 AC2990 30 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 2 from Patent WO9720068.
DEFINITION AC2990
ACCESSION AC2990
VERSION AC2990.1 GI:3716862
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE
1
AUTHORS Oerum, H. and Seeger, C.
TITLE METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL Patent: WO 9720068-A 2 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES
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1..30
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/organism="unidentified"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x A62990 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 2
A62996/c AC2996 30 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 8 from Patent WO9720068.
DEFINITION AC2996
ACCESSION AC2996
VERSION AC2996.1 GI:3716868
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE
1
AUTHORS Oerum, H. and Seeger, C.
TITLE METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL Patent: WO 9720068-A 8 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES
source
1..30
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x A62996 (1-30)
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QY 139 ProProAlaArgProProProProProPro 148
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Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 3
ARI179065
LOCUS ARI179065 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 2 from patent US 6326143.
ACCESSION ARI179065
VERSION ARI179065.1 GI:20220620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Orum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 2 04-DEC-2001;
FEATURES
source
1..30
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x ARI179065 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
LOCUS 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 4
ARI179071/c
LOCUS ARI179071 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 8 from patent US 6326143.
ACCESSION ARI179071
VERSION ARI179071.1 GI:20220626
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Orum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 8 04-DEC-2001;
FEATURES
source
1..30
Location/Qualifiers
/mol_type="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x ARI179071 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
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Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 5
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CS130457
LOCUS CS130457 30 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 12 from Patent WO2005063300.
ACCESSION CS130457
VERSION CS130457.1 GI:71792424
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kippenberger,S.
TITLE Cosmetic or pharmaceutical preparations containing nucleic acid
JOURNAL sequences forming a superstructure
FEATURES Patent: WO 2005063300-A 12 14-JUL-2005;
source Phenion GmbH & Co KG (DE)
1..30 Location/Qualifiers
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/mol_type="phosphorothioate"

ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS130457 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
LOCUS 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 6
CS172228/c
LOCUS CS172228 30 bp DNA linear PAT 05-OCT-2005
DEFINITION Sequence 6 from Patent WO2005085476.
ACCESSION CS172228
VERSION CS172228.1 GI:77156889
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hahn,S.
TITLE Detection of strp, such as fragile x syndrome
JOURNAL Patent: WO 2005085476-A 6 15-SEP-2005;
FEATURES Biocept, Inc. (US)
source Location/Qualifiers
1..30
/mol_type="unassigned DNA"
/mol_type="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS172228 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
LOCUS 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30
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CS130457
LOCUS CS130457 30 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 12 from Patent WO2005063300.
ACCESSION CS130457
VERSION CS130457.1 GI:71792424
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kippenberger,S.
TITLE Cosmetic or pharmaceutical preparations containing nucleic acid
JOURNAL sequences forming a superstructure
FEATURES Patent: WO 2005063300-A 12 14-JUL-2005;
source Phenion GmbH & Co KG (DE)
1..30 Location/Qualifiers
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/mol_type="phosphorothioate"

ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS130457 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
LOCUS 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 6
CS172228/c
LOCUS CS172228 30 bp DNA linear PAT 05-OCT-2005
DEFINITION Sequence 6 from Patent WO2005085476.
ACCESSION CS172228
VERSION CS172228.1 GI:77156889
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hahn,S.
TITLE Detection of strp, such as fragile x syndrome
JOURNAL Patent: WO 2005085476-A 6 15-SEP-2005;
FEATURES Biocept, Inc. (US)
source Location/Qualifiers
1..30
/mol_type="unassigned DNA"
/mol_type="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.54e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS172228 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
LOCUS 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30
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Db 30 CCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1

RESULT 7

AR202764

LOCUS I84402 30 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 12 from patent US 6365344.

ACCESSION AR202764

VERSION AR202764.1 GI:21498978

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Nolan,G.P. and Rothenberg,S.Michael.

TITLE Methods for screening for transdominant effector peptides and RNA molecules

JOURNAL Patent: US 6365344-A 12 02-APR-2002;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.54e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservative: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR202764 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148

Db 1 CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 30

RESULT 8

AR202764

LOCUS I84401 30 bp DNA linear PAT 04-APR-1998

DEFINITION Sequence 2 from patent US 5695933.

ACCESSION I84401

VERSION I84401.1 GI:3021921

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Schalling,M., Hudson,T.J. and Housman,D.E.

TITLE Direct detection of expanded nucleotide repeats in the human genome

JOURNAL Patent: US 5695933-A 2 09-DEC-1997;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.54e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservative: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I84401 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148

Db 1 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30

RESULT 9

I84402

LOCUS I84402 30 bp DNA linear PAT 04-APR-1998

DEFINITION Sequence 3 from patent US 5695933.

ACCESSION I84402

VERSION I84402.1 GI:3021922

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Schalling,M., Hudson,T.J. and Housman,D.E.

TITLE Direct detection of expanded nucleotide repeats in the human genome

JOURNAL Patent: US 5695933-A 3 09-DEC-1997;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.54e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservative: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I84402 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148

Db 30 CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1

RESULT 11

AX104904

LOCUS AX104904 30 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 1096 from Patent WO0122972.

ACCESSION AX104904

VERSION AX104904.1 GI:13921101

KEYWORDS

RESULT 13	BD169736	28 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD169736/c				
DEFINITION	C-terminus modified protein and process for producing the same, modifier and translational plate usable in producing C-terminus modified protein, and method of detecting protein interaction by using C-terminus modified protein.				
ACCESSION	BD169736				
VERSION	BD169736.1	GI:27875548			
KEYWORDS	WO 0246395-A/27				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 28)				
AUTHORS	Yanagawa,H., Doi,N., Miyamoto,E., Hideaki, Takashima and Oyama,R.				
TITLE	C-terminus modified protein and process for producing the same, modifier and translational plate usable in producing C-terminus modified protein, and method of detecting protein interaction by using C-terminus modified protein				
JOURNAL	Patent: WO 0246395-A 27 13-JUN-2002;				
	KEIO UNIVERSITY,HIROSHI YANAGAWA,NOBUHIDE DOI,ETSUKO MIYAMOTO, HIDEAKI TAKASHIMA,RIEKO OYAMA				
COMMENT	OS Artificial Sequence				
	PN WO 0246395-A/27				
	PD 13-JUN-2002				
	PF 07-DEC-2001 WO 2001JP010731				
	PR 07-DEC-2000 JP 00P 373105				
	PI HIROSHI YANAGAWA,NOBUHIDE DOI,ETSUKO MIYAMOTO,HIDEAKI PI TAKASHIMA,RIEKO OYAMA				
	PC C12N15/09,C07K1/13,C12P21/02				
	CC PCR primer containing part of c-jun and 8-repeated His-tags FH				
Key	FT source	1..28	Location/Qualifiers		
FT	Location/Qualifiers		/organism='Artificial Sequence'.		
FEATURES	source	1..28	Location/Qualifiers		
			/organism="synthetic construct"		
			/mol_type="genomic DNA"		
			/db_xref="taxon:32630"		
ORIGIN					
Alignment Scores:					
Pred. No.:	1.01e+05	Length:	28		
Score:	50.00	Matches:	9		
Percent Similarity:	81.8%	Conservative:	0		
Best Local Similarity:	81.8%	Mismatches:	0		
Query Match:	2.6%	Indels:	2		
DB:	2	Gaps:	1		
US-09-544-776-2 (1-373) x	BD169736 (1-28)				
Qy	138	GluProProAlaArgProProProProPro	148		
Db	28	GAACACCA-----CCACCA	CACCA		
RESULT 14	AR534150/c				
LOCUS	AR534150	30 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	Sequence 397 from patent US 6733965.				
ACCESSION	AR534150				
VERSION	AR534150.1	GI:53924183			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 30)				
AUTHORS	Echt,C.S. and Nelson,C.D.				
TITLE	Microsatellite DNA markers and uses thereof				
JOURNAL	Patent: US 6733965-A 397 11-MAY-2004;				
	International Paper Company and The United States of America as represented by the Secretary of Agriculture; Purchase, NY				
FEATURES	Location/Qualifiers				

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source 1.30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.09e+05 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR534150 (1-30)

Qy 34 GluGluGluGluGluGluGluGlu 43
Db 30 GAAGAAGAAGAAGAAGAAGAAGAAGA 1

RESULT 15
LOCUS I06458 28 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent WO 9001065.
ACCESSION I06458
VERSION I06458.1 GI:589699
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 28)
AUTHORS Fry, K., Larrick, J. and Tam, A.
TITLE RNA AND DNA AMPLIFICATION TECHNIQUES
JOURNAL Patent: WO 9001065-A 1 08-FEB-1990;
FEATURES
source
1.28
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.29e+05 Length: 28
Score: 48.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I06458 (1-28)

Qy 141 AlaArgProProProProPro 148
Db 3 TCTAGACCCGCCGCCGCCGCCGCC 26

RESULT 16
LOCUS AR365493 25 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 3 from patent US 5504194.
ACCESSION AR365493
VERSION AR365493.1 GI:34429214
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS St. John, T.P., Gallatin, W.M. and Idzerda, R.L.
TITLE Lymphocyte adhesion receptor for high endothelium, CD44
JOURNAL Patent: US 5504194-A 3 02-APR-1996;
FEATURES
source
1.25
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

, ORIGIN

Alignment Scores:
Pred. No.: 1.3e+05 Length: 25
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR365493 (1-25)

Qy 142 ArgProProProProProPro 148
Db 5 CGGCGGCCGCCGCCGCCGCCGCC 25

RESULT 17
LOCUS AR534108 30 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 355 from patent US 6733965.
ACCESSION AR534108
VERSION AR534108.1 GI:53924141
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Echt, C.S. and Nelson, C.D.
TITLE Microsatellite DNA markers and uses thereof
JOURNAL Patent: US 6733965-A 355 11-MAY-2004;
International Paper Company and The United States of America as
represented by the Secretary of Agriculture; Purchase, NY
FEATURES
source
1.30
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.56e+05 Length: 30
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR534108 (1-30)

Qy 143 ProProProProProProAlaSer 150
Db 2 CCACCACCACCACCACCACCATCATCA 25

RESULT 18
LOCUS E04986 27 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence of 3'terminal fragment of ITR.
ACCESSION E04986
VERSION E04986.1 GI:2173181
KEYWORDS JP 1993103673-A/80.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Sengu, K.Y. and Ito, S.
TITLE REPLICATION OF DNA
JOURNAL Patent: JP 1993103673-A 80 27-APR-1993;
ARIZONA BOARD OF REGENTS
OS Artificial gene
COMMENT OC Artificial sequence; Genes.
PN JP 1993103673-A/80
PD 27-APR-1993
PF 26-AUG-1991 JP 1991240525
PI SENGU KUU YUU, ITO SUMIYOSHI
PC C12N15/10, C12N15/11//C12Q1/68;
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CC strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FH
 FT misc_feature 1..27
 FT /notes='3'terminal fragment of ITR'.
 FT Location/Qualifiers
 FT 1..27
 FT /organism='synthetic construct'
 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:32630'

FEATURES

source
 ORIGIN

Alignment Scores:
 Pred. No.: 1.58e+05 Length: 27
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x E04986 (1-27)

QY 139 ProProAlaArgProProProPro 147

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 19
 E04987/c
 LOCUS 27 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of 3'terminal fragment of ITR.
 ACCESSION E04987
 VERSION E04987.1 GI:2173182
 KEYWORDS JP 1993103673-A/81.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Sengu,K.Y. and Ito,S.
 TITLE REPLICATION OF DNA
 JOURNAL PATENT: JP 1993103673-A 81 27-APR-1993;
 ARIZONA BOARD OF REGENTS
 COMMENT OS Artificial gene
 OC Artificial sequence; Genes.
 PN JP 1993103673-A/81
 PD 27-APR-1993

PF 26-AUG-1991 JP 1991240525
 PI SENGU KUU YUU, ITO SUMIYOSHI
 PC C12N15/10, C12N15/11//C12Q1/68;
 CC strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FH
 FT misc_feature 1..27
 FT /notes='3'terminal fragment of ITR'.
 FT Location/Qualifiers
 FT 1..27
 FT /organism='synthetic construct'
 FT /mol_type='genomic DNA'
 FT /db_xref='taxon:32630'

FEATURES

source
 ORIGIN

Alignment Scores:
 Pred. No.: 1.58e+05 Length: 27
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x E04987 (1-27)

QY 139 ProProAlaArgProProProPro 147

Db 27 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 20
 ARI20087/c
 LOCUS 28 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 1 from patent US 6153596.
 ACCESSION ARI20087
 VERSION ARI20087.1 GI:14102786
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 ORIGIN

REFERENCE 1 (bases 1 to 28)
 AUTHORS Liotta,D.C., Petros,J.A., Wey,S.-J., Karr,J.F. and Pohl,J.
 TITLE Polycationic oligomers
 JOURNAL Patent: US 6153596-A 1 28-NOV-2000;
 FEATURES Location/Qualifiers
 source
 1..28
 /organism='unknown'
 /mol_type='unassigned DNA'

ORIGIN

Alignment Scores:
 Pred. No.: 1.64e+05 Length: 28
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x ARI20087 (1-28)

QY 139 ProProAlaArgProProProPro 147

Db 27 CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1

RESULT 21
 E44025/c
 LOCUS 28 bp DNA linear PAT 31-JAN-2002
 DEFINITION Novel human gene analogous to secretory mouse protein sFRP-1.
 ACCESSION E44025
 VERSION E44025.1 GI:18625177
 KEYWORDS JP 2000106889-A/3.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Fu,A. and Zu,Y.
 TITLE Novel human gene analogous to secretory mouse protein sFRP-1
 JOURNAL Patent: JP 2000106889-A 3 18-APR-2000;
 SMITHKLINE BEECHAM CORP

COMMENT
 OS Unidentified
 PN JP 2000106889-A/3
 PD 18-APR-2000
 PF 10-SEP-1999 JP 1999256823
 PR 08-AUG-1997 US 08/907808,23-MAY-1997 US 60/047691 PI

ADINGU FU,YUAN ZU
 PC C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395, PC
 A61K39/395,A61K45/00,
 PC A61K48/00,A61P3/04,A61P3/10,A61P9/00,A61P9/12,A61P13/12, PC
 C07K14/47,
 PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, PC
 C12Q1/02, C12Q1/68,
 PC G01N33/53, G01N33/531, G01N33/566, G01N33/577//C12P21/08, PC
 C12N15/00,A61K37/02,
 PC C12N5/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..28
 FT /organism='Unidentified'.
 FT Location/Qualifiers

FEATURES

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x E44025 (1-28)
Qy 143 ProProProProProProAala 149
Db 28 CCGCGCGCGCGCGCGCGCGCA 8

RESULT 22
I41109
LOCUS I41109 28 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 12 from patent US 5624803.
ACCESSION I41109
VERSION I41109.1 GI:2081699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the
binding affinity of triplex forming oligonucleotides derived
therefrom
JOURNAL Patent: US 5624803-A 12 29-APR-1997;
FEATURES Location/Qualifiers
source 1. .28
/organism="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I41109 (1-28)
Qy 140 ProAlaArgProProProProPro 148
Db 2 CCTCTCTCTCTCTCTCTCTCTCTCTCTCC 28

RESULT 23
I41110/c
LOCUS I41110 28 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 13 from patent US 5624803.
ACCESSION I41110
VERSION I41110.1 GI:2081700
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the
binding affinity of triplex forming oligonucleotides derived
therefrom
JOURNAL Patent: US 5624803-A 13 29-APR-1997;
FEATURES Location/Qualifiers
source 1. .28
/organism="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I41113 (1-28)
Qy 140 ProAlaArgProProProProPro 148
Db 2 CCTCTCTCTCTCTCTCTCTCTCTCTCTCC 28

RESULT 25
I41118
LOCUS I41118 28 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 21 from patent US 5624803.
ACCESSION I41118
VERSION I41118.1 GI:2081708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the
binding affinity of triplex forming oligonucleotides derived
therefrom
JOURNAL Patent: US 5624803-A 21 29-APR-1997;
FEATURES Location/Qualifiers
source 1. .28
/organism="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I41113 (1-28)
Qy 140 ProAlaArgProProProProPro 148
Db 2 CCTCTCTCTCTCTCTCTCTCTCTCTCTCC 28

RESULT 24
I41113
LOCUS I41113 28 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 16 from patent US 5624803.
ACCESSION I41113
VERSION I41113.1 GI:2081703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the
binding affinity of triplex forming oligonucleotides derived
therefrom
JOURNAL Patent: US 5624803-A 16 29-APR-1997;
FEATURES Location/Qualifiers
source 1. .28
/organism="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x I41110 (1-28)
Qy 140 ProAlaArgProProProProPro 148
Db 27 CCTCTCTCTCTCTCTCTCTCTCTCTCTCC 1
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source
1. .28
/organism="synthetic construct"
/motif_name="unsequenced DNA"
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/db xref="taxon:32630"
/note="Synthetic oligonucleotide
phosphorothioate backbone"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AX355143 (1-28)

Qy 139 ProProAlaArgProProProPro 147
|||||
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 30
AX547631 AX547631 28 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 770 from Patent WO2053141.
ACCESSION AX547631
VERSION AX547631.1 GI:25812775
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Bratzler R.L.
TITLE
Inhibition of angiogenesis by nucleic acids
JOURNAL
Patent: WO 02053141-A 770 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AX547631 (1-28)

Qy 139 ProProAlaArgProProProPro 147
|||||
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 31
BD252103/c
LOCUS BD252103 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Antiproliferative activity of G-rich oligonucleotides and method of
using same to bind to nucleoboln.
ACCESSION BD252103
VERSION BD252103.1 GI:33061873
KEYWORDS
SOURCE JP 2002541264-A/7.
unidentified
ORGANISM unclassified sequences.
1 (bases 1 to 29)
REFERENCE
1
AUTHORS Miller,D.M., Bates,P.J. and Trent,J.O.
TITLE Antiproliferative activity of G-rich oligonucleotides and method of
using same to bind to nucleoboln
JOURNAL Patent: JP 2002541264-A 7 03-DEC-2002;
THE UAB RESEARCH FOUNDATION

COMMENT OS Other nucleic acid
PN JP 2002541264-A/7
PD 03-DEC-2002
PF 07-APR-2000 JP 2000610866
PR 08-APR-1999 US 60/149823 PI
DONALD M MILLER, PAULA J BATES, JOHN O TRENT
PC A61K31/711,A61K31/136,A61K31/337,A61K31/475,A61K31/513,A61K31/
PC 522,
PC
A61K31/573,A61K31/7048,A61K33/24,A61K45/00,A61P35/00,A61P43/00, PC
Cl2Q1/04,
PC GOIN33/15,GOIN33/50,GOIN33/53,GOIN33/566
CC Antiproliferative activity of G-rich oligonucleotides and CC
method of using
CC same to bind to nucleoboln
FH Key Location/Qualifiers
FT source 1..29
/organism="Other nucleic acid".
FEATURES
source
1..29
Location/Qualifiers
1..29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 1.7e+05 Length: 29
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x BD252103 (1-29)

Qy 139 ProProAlaArgProProProPro 147
|||||
Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 32
CS077885/c
LOCUS CS077885 29 bp DNA linear PAT 06-MAY-2005
DEFINITION Sequence 3 from Patent WO2005035579.
ACCESSION CS077885
VERSION CS077885.1 GI:63092973
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Bates,P.J., Miller,D.M., Trent,J.O. and Xu,X.
TITLE A method for the treatment of malignant diseases by inhibiting
nucleoboln
JOURNAL Patent: WO 2005035579-A 3 21-APR-2005;
University of Louisville Research Foundation (US)
FEATURES
source
1..29
Location/Qualifiers
1..29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Synthetic
polynucleotide sequence"

ORIGIN
Alignment Scores:
Pred. No.: 1.7e+05 Length: 29
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS077885 (1-29)
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QY 139 ProProAlaArgProProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 33
LOCUS CS097965/c 29 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 3 from Patent WO2005037323.
ACCESSION CS097965
VERSION CS097965.1 GI:66954210
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bates,P.J., Girvan,A.C. and Barve,S.S.
TITLE Method for inhibiting nf-kappa b signaling and use to treat or prevent human diseases
JOURNAL Patent: WO 2005037323-A 3 28-APR-2005;
University of Louisville Research Foundation, Inc. (US)
FEATURES Location/Qualifiers
source 1..29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="description of Artificial Sequence: Synthetic polynucleotide sequence"

ORIGIN
Alignment Scores: Length: 29
Pred. No.: 1.7e+05
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservatives: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x CS097965 (1-29)

QY 139 ProProAlaArgProProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 34
LOCUS AR016486/c 30 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5776744.
ACCESSION AR016486
VERSION AR016486.1 GI:3972763
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Glazer,P.M., Lin,L.,Michael, and George,J.
TITLE Methods and compositions for effecting homologous recombination
JOURNAL Patent: US 5776744-A 1 07-JUL-1998;
Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: Length: 30
Pred. No.: 1.76e+05
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservatives: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AR016486 (1-30)

QY 139 ProProAlaArgProProProProProAla 149
Db 28 CCCCCT-----CCCCCACCACCCCCCTTCC 2

RESULT 35
LOCUS AR078334/c 30 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5962426.
ACCESSION AR078334
VERSION AR078334.1 GI:10005080
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Glazer,P.M.
TITLE Triple-helix forming oligonucleotides for targeted mutagenesis
JOURNAL Patent: US 5962426-A 3 05-OCT-1999;
Location/Qualifiers
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: Length: 30
Pred. No.: 1.76e+05
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservatives: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AR078334 (1-30)

QY 139 ProProAlaArgProProProProProAla 149
Db 28 CCCCCT-----CCCCCACCACCCCTTCC 2

RESULT 36
LOCUS AR173054/c 30 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6303376.
ACCESSION AR173054
VERSION AR173054.1 GI:17912545
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Glazer,P.M.
TITLE Methods of targeted mutagenesis using triple-helix forming oligonucleotides
JOURNAL Patent: US 6303376-A 3 16-OCT-2001;
Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: Length: 30
Pred. No.: 1.76e+05
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservatives: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AR173054 (1-30)

QY 139 ProProAlaArgProProProProProAla 149
Db 28 CCCCCT-----CCCCCACCACCCCTTCC 2

RESULT 37
E04679/c
LOCUS
DEFINITION Synthetic nucleotide with (GACGTC) structure, having immunomodulation activities.
ACCESSION E04679
VERSION E04679.1 GI:2172875
KEYWORDS JP 1992352724-A/36.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O., Makino,T. and Shimada,S.
TITLE IMMUNOMODULATION TYPE THERAPEUTIC AGENT
JOURNAL Patent: JP 1992352724-A 36 07-DEC-1992;
MITSUI TOATSU CHEM INC
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
FN JP 1992352724-A/36
PD 07-DEC-1992
PR 18-JUL-1991 JP 1991178058
PI 27-JUL-1990 JP 90P 197778
PI TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO ETSURO,
PI YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
PC A61K31/70,A61K31/70,A61K31/70//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT misc_feature 1..30
FT /note='synthetic nucleotide with (GACGTC) structure'.
FT
FT
FEATURES
source
1..30
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0
US-09-544-776-2 (1-373) x E04679 (1-30)
Qy 139 ProProAlaArgProProProPro 146
Db 25 CCCCCCGACGTCCTCCCCCCCCC 2
RESULT 38
E04682
LOCUS
DEFINITION Synthetic nucleotide with (GACGTC) structure, having immunomodulation activities.
ACCESSION E04682
VERSION E04682.1 GI:2172878
KEYWORDS JP 1992352724-A/39.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O., Makino,T. and Shimada,S.
TITLE IMMUNOMODULATION TYPE THERAPEUTIC AGENT

JOURNAL Patent: JP 1992352724-A 39 07-DEC-1992;
MITSUI TOATSU CHEM INC
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
FN JP 1992352724-A/39
PD 07-DEC-1992
PR 18-JUL-1991 JP 1991178058
PI 27-JUL-1990 JP 90P 197778
PI TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO ETSURO,
PI YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
PC A61K31/70,A61K31/70,A61K31/70//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT misc_feature 1..30
FT /note='synthetic nucleotide with (GACGTC) structure'.
FT
FT
FEATURES
source
1..30
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0
US-09-544-776-2 (1-373) x E04682 (1-30)
Qy 139 ProProAlaArgProProProPro 146
Db 6 CCCCCCGACGTCCTCCCCCCCCC 29
RESULT 39
AR202765/c
LOCUS AR202765 30 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6365344.
ACCESSION AR202765
VERSION AR202765.1 GI:21498979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Nolan,G.P. and Rothenberg,S.Michael.
TITLE Methods for screening for transdominant effector peptides and RNA molecules
JOURNAL Patent: US 6365344-A 13 02-APR-2002;
FEATURES Location/Qualifiers
source
1..30
/organism='unknown'
/mol_type='unassigned DNA'
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0
US-09-544-776-2 (1-373) x AR202765 (1-30)

```
QY 139 ProProAlaArgProProProProPro 147
Db 29 CCNCNCNCNCNCNCNCNCNCNCNCN 3

RESULT 40
AR242044/c
LOCUS AR242044 30 bp DNA
DEFINITION Sequence 332 from patent US 6472154.
ACCESSION AR242044
VERSION AR242044.1 GI:27287856
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 332 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR242044 (1-30)

QY 139 ProProAlaArgProProProProPro 147
Db 29 CGCGCGCGCGCGCGCGCGCGCGCG 3

RESULT 41
AR306619
LOCUS AR306619 30 bp DNA
DEFINITION Sequence 10 from patent US 6548642.
ACCESSION AR306619
VERSION AR306619.1 GI:31696821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 10 15-APR-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR306619 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 42
AR306628
LOCUS AR306628 30 bp DNA
DEFINITION Sequence 38 from patent US 6548642.
ACCESSION AR306628
VERSION AR306628.1 GI:31696830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 38 15-APR-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR306628 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 43
AR340054
LOCUS AR340054 30 bp DNA
DEFINITION Sequence 10 from patent US 6570062.
ACCESSION AR340054
VERSION AR340054.1 GI:33731348
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 10 27-MAY-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR340054 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 44
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QY 139 ProProAlaArgProProProProPro 147
Db 29 CCNCNCNCNCNCNCNCNCNCNCNCN 3

RESULT 40
AR242044/c
LOCUS AR242044 30 bp DNA
DEFINITION Sequence 332 from patent US 6472154.
ACCESSION AR242044
VERSION AR242044.1 GI:27287856
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 332 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR242044 (1-30)

QY 139 ProProAlaArgProProProProPro 147
Db 29 CGCGCGCGCGCGCGCGCGCGCGCG 3

RESULT 41
AR306619
LOCUS AR306619 30 bp DNA
DEFINITION Sequence 10 from patent US 6548642.
ACCESSION AR306619
VERSION AR306619.1 GI:31696821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 10 15-APR-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR306619 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 42
AR306628
LOCUS AR306628 30 bp DNA
DEFINITION Sequence 38 from patent US 6548642.
ACCESSION AR306628
VERSION AR306628.1 GI:31696830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 38 15-APR-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR306628 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 43
AR340054
LOCUS AR340054 30 bp DNA
DEFINITION Sequence 10 from patent US 6570062.
ACCESSION AR340054
VERSION AR340054.1 GI:33731348
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 10 27-MAY-2003;
Ohio University; Athens, OH
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AR340054 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 44
```

AR340063 AR340063 30 bp DNA PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 38 from patent US 6570062.
ACCESSION AR340063
VERSION AR340063.1 GI:33731357
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6570062-A 38 27-MAY-2003;
Ohio University; Athens, OH
FEATURES
source
1. .30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 0
US-09-544-776-2 (1-373) x AR340063 (1-30)
Qy 139 ProProAlaArgProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30
RESULT 45
AR412123 AR412123 30 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 10 from patent US 6639050.
ACCESSION AR412123
VERSION AR412123.1 GI:40166767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 10 28-OCT-2003;
Ohio University; Athens, OH
FEATURES
source
1. .30
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 0
US-09-544-776-2 (1-373) x AR412123 (1-30)
Qy 139 ProProAlaArgProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30
RESULT 46
AR412132 AR412132 30 bp DNA PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 38 from patent US 6639050.
ACCESSION AR412132
VERSION AR412132.1 GI:40166776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 38 28-OCT-2003;
Ohio University; Athens, OH
FEATURES
source
1. .30
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.76e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
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ORGANISM Unknown.
REFERENCE Unclassified.
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AUTHORS Rouleau, G.A. and Brais, B.
TITLE Short GCG expansions in the PAB II gene for oculopharyngeal muscular dystrophy and diagnostic thereof
JOURNAL Patent: US 6828430-A 4 07-DEC-2004;
McGill University; Montreal; WOX;
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REFERENCE Unclassified.
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AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6570062-A 38 27-MAY-2003;
Ohio University; Athens, OH
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ORGANISM Unknown.
REFERENCE Unclassified.
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AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 10 28-OCT-2003;
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ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Kieliszewski, M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 38 28-OCT-2003;
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DEFINITION Sequence 4 from patent US 6828430.
ACCESSION AR614765
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1 (bases 1 to 30)
AUTHORS Rouleau, G.A. and Brais, B.
TITLE Short GCG expansions in the PAB II gene for oculopharyngeal muscular dystrophy and diagnostic thereof
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ORGANISM Unknown.
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AUTHORS Zhong, W., Hong, Z. and Ferrari, E.
TITLE HCV replicase complexes
JOURNAL Patent: US 6967075-A 7 22-NOV-2005;
Schering Corporation; Kenilworth, NJ
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KEYWORDS
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AUTHORS Reiml, S.J., Lindbo, J.A. and Turpen, T.
TITLE Creation of variable length and sequence linker regions for
dual-domain or multi-domain molecules
JOURNAL Patent: WO 0123543-A 36 05-APR-2001;
Large Scale Biology Corporation (US)
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VERSION AX267025.1 GI:16515810
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
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AUTHORS Seidman, M.M. and Majumdar, A.
TITLE Establishment of cellular manipulations which enhance
oligo-mediated gene targeting
JOURNAL Patent: WO 0173001-A 14 04-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
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; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
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; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia

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; APPLICANT: Seeger, Corina
; TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
; FILE REFERENCE: sequence listing
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; CURRENT FILING DATE: 1998-05-22
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; EARLIER FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-8

Alignment Scores:
Pred. No.: 7.76e+03 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-083-123-8 (1-30)
QY 139 ProProAlaArgProProProProPro 148
Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 6
US-08-589-109A-12
; Sequence 12, Application US/08589109A
; Patent No. 6365344
; GENERAL INFORMATION:
; APPLICANT: No. 6365344an, Garry P.
; APPLICANT: Rothenberg, Michael S.
; TITLE OF INVENTION: Methods for Screening for Transdominant
; TITLE OF INVENTION: Effector Peptides and RNA Molecules
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,109A
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-589-109A-12

Alignment Scores:
Pred. No.: 7.76e+03 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-589-109A-12 (1-30)
QY 139 ProProAlaArgProProProProPro 148
Db 1 CCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 30

RESULT 7
US-09-232-785-397/c
; Sequence 397, Application US/09232785
; Patent No. 6733965
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig S.
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 4481/1E188US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-397

Alignment Scores:
Pred. No.: 1.23e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-232-785-397 (1-30)
QY 34 GluGluGluGluGluGluGluGluGlu 43
Db 30 GAAGAAGAGAGAGAGAGAGAGAGAGAGAA 1

RESULT 8
5504194-3
; Patent No. 5504194
; APPLICANT: ST. JOHN, THOMAS P.; GALLATIN, W. MICHAEL; IDZERDA,
; REJEAN
; TITLE OF INVENTION: LYPHOCYTE ADHESION RECEPTOR FOR HIGH
; ENDOTHELIUM, CD44
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/884,624
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 628,646
; FILING DATE: 12-DEC-1990
; APPLICATION NUMBER: 325,224
; FILING DATE: 17-MAR-1989
; SEQ ID NO:3:
```



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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602) 956-7000
; TELEFAX: (602) 495-9475
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-208-486-80

Alignment Scores:
Pred. No.: 1.97e+04 Length: 27
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-08-208-486-80 (1-27)
QY 139 ProProAlaArgProProProPro 147
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 12
US-08-208-486-81/c
; Sequence 81, Application US/08208486
; Patent No. 5389531
; GENERAL INFORMATION:
; APPLICANT: Ito, Junetsu
; APPLICANT: Ito, Seung-Ku
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING
; TITLE OF INVENTION: PRDI-CATALYZED DNA REPLICATION SYSTEMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cahill, Sutton & Thomas
; STREET: 155 Park One, 2141 E. Highland Ave.
; CITY: Phoenix
; STATE: Arizona
; COUNTRY: U.S.A.
; ZIP: 85016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: Packard Bell (IBM PC/AT compatible)
; OPERATING SYSTEM: MS-Dos, Version 5.0
; SOFTWARE: WordPerfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,486
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,916
; FILING DATE: April 14, 1992
; APPLICATION NUMBER: Japan 240525/91
; FILING DATE: August 26, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janelle Faunce Raupp
; REGISTRATION NUMBER: 30,485
; REFERENCE/DOCKET NUMBER: #3954-A-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602) 956-7000
; TELEFAX: (602) 495-9475
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-208-486-81

```

```

Alignment Scores:
Pred. No.: 1.97e+04 Length: 27
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-08-208-486-81 (1-27)
QY 139 ProProAlaArgProProProPro 147
Db 27 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 13
US-08-324-001-12
; Sequence 12, Application US/08324001
; Patent No. 5624803
; GENERAL INFORMATION:
; APPLICANT: NOONBERG, SARAH B.
; APPLICANT: HUNT, C. ANTHONY
; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,001
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 22000-20544.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSN FOERSFO
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-324-001-12

Alignment Scores:
Pred. No.: 2.06e+04 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-08-324-001-12 (1-28)
QY 140 ProAlaArgProProProProPro 148
Db 2 CCUCUCCUCCUCCUCCUCCUCCUCC 28

RESULT 14
US-08-324-001-13/c

```

Sequence 13, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 13:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-324-001-13

Alignment Scores:
Pred. No.: 2.06e+04 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x US-08-324-001-13 (1-28)

QY 140 ProAlaArgProProProProProPro 148
Db 27 CCTCTCTCTCTCTCTCTCTCTCTCTCTCC 1

RESULT 15

US-08-324-001-16
Sequence 16, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 16:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-324-001-16

Alignment Scores:
Pred. No.: 2.06e+04 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x US-08-324-001-16 (1-28)

QY 140 ProAlaArgProProProProProPro 148
Db 2 CCUCUCCUCCUCCUCCUCCUCCUCC 28

RESULT 16

US-08-324-001-21
Sequence 21, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792

; TELEX: 706141 MRSN FOERSSFO
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-324-001-21

Alignment Scores: 2.06e+04 Length: 28
Pred. No.: 46.00 Matches: 7
Score: 77.8% Conservative: 0
Percent Similarity: 77.8% Mismatches: 2
Best Local Similarity: 77.8% Indels: 0
Query Match: 2.4% Gaps: 0
DB: 2

US-09-544-776-2 (1-373) x US-08-324-001-21 (1-28)

Qy 140 ProAlaA:rgProProProProPro 148
Db 2 CCUCUCCUCCUCCUCCUCCUCC 28

RESULT 17

US-08-324-001-22/c
; Sequence 22, Application US/08324001
; Patent No. 5624803
; GENERAL INFORMATION:
; APPLICANT: NOONBERG, SARAH B.
; APPLICANT: HUNT, C. ANTHONY
; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,001
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 22000-20544.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSN FOERSSFO
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-324-001-22

Alignment Scores: 2.06e+04 Length: 28
Pred. No.: 46.00 Matches: 7
Score: 77.8% Conservative: 0
Percent Similarity: 77.8% Mismatches: 2
Best Local Similarity: 77.8% Indels: 0
Query Match: 2.4% Gaps: 0
DB: 2

US-09-544-776-2 (1-373) x US-08-324-001-22 (1-28)
Qy 140 ProAlaA:rgProProProProPro 148
Db 27 CCTCTCTCTCTCTCTCTCTCTCTCTCC 1

RESULT 18

US-08-846-020A-2/c
; Sequence 2, Application US/08846020A
; Patent No. 6090547
; GENERAL INFORMATION:
; APPLICANT: Drazen M.D., Jeffrey M.
; APPLICANT: In M.D., Kwang-Ho
; APPLICANT: Asano M.D., Koichiro
; APPLICANT: Beier, David
; APPLICANT: Grobholz, James
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
; TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,020A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0092662-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248 4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: 12 base pair deletion
US-08-846-020A-2

Alignment Scores: 2.06e+04 Length: 28
Pred. No.: 46.00 Matches: 8
Score: 81.8% Conservative: 1
Percent Similarity: 81.8% Mismatches: 0
Best Local Similarity: 72.7% Indels: 2
Query Match: 2.4% Gaps: 1
DB: 3

US-09-544-776-2 (1-373) x US-08-846-020A-2 (1-28)

Qy 139 ProProAlaA:rgProProProProProAla 149
Db 27 CCCCCG-----CCCCCGCCCCCGCCCGTCG 1

RESULT 19

US-08-993-008A-1/c
; Sequence 1, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:

APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shioh-Jyi
APPLICANT: Karr, Joan F.
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
US-08-993-008A-1

Alignment Scores:
Pred. No.: 2.06e-04 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-993-008A-1 (1-28)

QY 139 ProProAlaArgProProProPro 147
Db 27 CCTCTCTCTCTCTCTCTCTCTCTCC 1

RESULT 20
US-09-617-871-2/c
Sequence 2, Application US/09617871
Patent No. 6355434
GENERAL INFORMATION:
APPLICANT: Drazen M.D., Jeffrey M.
APPLICANT: In M.D., Kwang-Ho
APPLICANT: Asano M.D., Koichiro
APPLICANT: Beier, David
APPLICANT: Grobholz, James
TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART

STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/617,871
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,020
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0092662-0012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248 4000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: 12 base pair deletion
US-09-617-871-2

Alignment Scores:
Pred. No.: 2.06e+04 Length: 28
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x US-09-617-871-2 (1-28)

QY 139 ProProAlaArgProProProProAla 149
Db 27 CCCCCG-----CCCCCGCCCCCGCGTCG 1

RESULT 21
PCT-US92-09202-7/c
Sequence 7, Application PC/TUS9209202
GENERAL INFORMATION:
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Triplex Forming Oligonucleotide Reagents Targeted
TITLE OF INVENTION: to the Neu Oncogene Promoter and Method of Use
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09202
FILING DATE: 19921028
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5393
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Triplex forming oligonucleotide
HYPOTHETICAL: YES
PCT-US92-09202-7

Alignment Scores:
Pred. No.: 2,066+04 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x PCT-US92-09202-7 (1-28)

QY 140 ProAlaArgProProProProPro 148
Db 27 CCACACACCACACCACACCACCC 1

RESULT 22
US-08-467-126-1/c
Sequence 1, Application US/08467126
Patent No. 5776744
GENERAL INFORMATION:
APPLICANT: GLAZER, PETER M.
APPLICANT: GEORGE, JAY
APPLICANT: LIN, L. MICHAEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
EFFECTING HOMOLOGOUS RECOMBINATION
TITLE OF INVENTION: EFFECTING HOMOLOGOUS RECOMBINATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONCORPHARM, INC.
STREET: 200 PERRY PARKWAY
CITY: GAITHERSBURG
STATE: MARYLAND
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE-3.50 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: APPLE MACINTOSH POWERBOOK 520
OPERATING SYSTEM: MACINTOSH
SOFTWARE: WORD PERFECT 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,126
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KARTA, GLENN E.
REGISTRATION NUMBER: 30,649
REFERENCE/DOCKET NUMBER: PA-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2058
TELEFAX: 301-208-6997
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-126-1

Alignment Scores:
Pred. No.: 2,25e+04 Length: 30
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x US-08-467-126-1 (1-30)

QY 139 ProProAlaArgProProProProProAla 149
Db 28 CCCCT-----CCCCCACCACCCCCCTTCC 2

RESULT 23
US-08-476-712-3/c
Sequence 3, Application US/08476712
Patent No. 5962426
GENERAL INFORMATION:
APPLICANT: Glazer, Peter, M.
TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
Targeted Mutagenesis
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,712
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YU114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-476-712-3

Alignment Scores:
Pred. No.: 2,25e+04 Length: 30
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x US-08-476-712-3 (1-30)

QY 139 ProProAlaArgProProProProProAla 149

Db 28 CCCCC-----CCCCCACCACCCCCCTTCC 2

RESULT 24

US-09-411-291-3/c
; Sequence 3, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; Targeted Mutagenesis

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: GA

COUNTRY: USA
ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/411,291

FILING DATE: 04-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,712

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: YU114

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-873-8794

TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-411-291-3

Alignment Scores:

Pred. No.: 2.25e+04 Length: 30

Score: 46.00 Matches: 8

Percent Similarity: 81.8% Conservative: 1

Best Local Similarity: 72.7% Mismatches: 0

Query Match: 2.4% Indels: 2

DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x US-09-411-291-3 (1-30)

QY 139 ProProAlaArgProProProProAla 149

Db 28 CCCCC-----CCCCCACCACCCCCCTTCC 2

RESULT 25

US-08-589-109A-13/c
; Sequence 13, Application US/08589109A
; Patent No. 6365344
; GENERAL INFORMATION:
; APPLICANT: No. 6365344an, Garry P.
; APPLICANT: Rothenberg, Michael S.
; TITLE OF INVENTION: Methods for Screening for Transdominant
; TITLE OF INVENTION: Effector Peptides and RNA Molecules

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/589,109A

FILING DATE: 23-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 949-8711

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc feature

LOCATION: 3..4

OTHER INFORMATION: /note= "The 'N' appearing at

position 3, as well as at positions 6, 9, 12, 15, 18, 21, 24

and 30, can be either A,C,T or G."

US-08-589-109A-13

Alignment Scores:

Pred. No.: 2.25e+04 Length: 30

Score: 46.00 Matches: 7

Percent Similarity: 77.8% Conservative: 0

Best Local Similarity: 77.8% Mismatches: 2

Query Match: 2.4% Indels: 0

DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-589-109A-13 (1-30)

QY 139 ProProAlaArgProProProPro 147

Db 29 CCNCCNCCNCCNCCNCCNCCNCCN 3

RESULT 26

US-09-475-947A-332/c

; Sequence 332, Application US/09475947A

; Patent No. 6472154

; GENERAL INFORMATION:

; APPLICANT: Garner, Harold R.

; APPLICANT: Wren, Jonathan D.

; APPLICANT: Minna, John D.

; TITLE OF INVENTION: Polymorphic Repeats in Human Genes

; FILE REFERENCE: UTSD0667

; CURRENT APPLICATION NUMBER: US/09/475,947A

; CURRENT FILING DATE: 1999-12-31

; NUMBER OF SEQ ID NOS: 346

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 332

; LENGTH: 30

; TYPE: DNA

; ORGANISM: human

US-09-475-947A-332

Alignment Scores:

Pred. No.:	2.35e+04	Length:	30
Score:	46.00	Matches:	7
Percent Similarity:	77.8%	Conservative:	0
Best Local Similarity:	77.8%	Mismatches:	2
Query Match:	2.4%	Indels:	0
DB:	3	Gaps:	0

US-09-544-776-2 (1-373) x US-09-475-947A-332 (1-30)

Qy 139 ProProAlaArgProProProPro 147
Db 29 CCGCGCGCGCGCGCGCGCGCGCG 3

RESULT 27

```

US-09-119-507B-10
; Sequence 10, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: NO. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthet
US-09-119-507B-10

```

Alignment Scores:		
Pred. No.:	2.25e+04	30
Score:	46.00	7
Percent Similarity:	70.0%	Conservative: 0
Best Local Similarity:	70.0%	Mismatches: 3
Query Match:	2.4%	Indels: 0
DB:	3	Gaps: 0

US-09-544-776-2 (1-373) x US-09-119-507B-10 (1-30)

Qy	139	ProProAlaArgProProProProProPro	148
Dβ	1	CCACCACCTTCACTCCACCCCCATCTCCA	30

RESULT 28

```

US-09-119-507B-38
; Sequence 38, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642a1 Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-38

```

Alignment Scores:	
Pred. No.:	2.25e+04
Score:	46.00
Percent Similarity:	70.0%
Best Local Similarity:	70.0%
Query Match:	2.4%
Length:	3
Matches:	7
Conservative:	0
Mismatches:	3
Indels:	0

DB:	3	Gaps:	0
US-09-544-776-2 (1-373) x US-09-119-507B-38 (1-30)			
Qy	139	ProProAlaArgProProProProProProPro 148	
Db	1	CCAGCAGCTTCACCTCCACCCCACTCCCA 30	

RESULT 29

```

US-08-897-556A-10
; Sequence 10, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-897-556A-10

```

Alignment Scores:					
Pred. No.:	2.25e+04	Length:	30		
Score:	46.00	Matches:	7		
Percent Similarity:	70.0%	Conservative:	0		
Best Local Similarity:	70.0%	Mismatches:	3		
Query Match:	2.4%	Indels:	0		
DS:	1	Gaps:	0		

US-09-544-776-2 (1-373) x US-08-897-556A-10 (1-30)

Qy 139 ProProAlaArgProProProProProProProPro 148
pB 1 CCACCACCTTACCTCCACCCCCCATCTCCA 30

RESULT 30

RECD: 30
 US-08-897-556A-38
 ; Sequence 38, Application US/08897556A
 ; Patent No. 6570062
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: KIELSEWSKI, MARCIA J.
 ; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
 ; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
 ; NUMBER OF SEQUENCES: 106
 ;

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MEDLEN & CARROLL, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/897,556A
;; APPLICATION NUMBER: US/08/897,556A
;; FILING DATE: 21-JUL-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CARROLL, PETER G
;; REGISTRATION NUMBER: 32,837
;; REFERENCE/DOCKET NUMBER: OHU-02908
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "DNA"
US-08-897-556A-38

Alignment Scores:
Pred. No.: 2.25e+04 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-897-556A-38 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 31

US-09-547-693-10
; Sequence 10, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-10

Alignment Scores:
Pred. No.: 2.25e+04 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0

Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-547-693-10 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 32

US-09-547-693-38
; Sequence 38, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-38

Alignment Scores:
Pred. No.: 2.25e+04 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-547-693-38 (1-30)

QY 139 ProProAlaArgProProProProPro 148
Db 1 CCACCACCTTCACCTCCACCCCATCTCCA 30

RESULT 33

US-09-590-211A-4/c
; Sequence 4, Application US/09590211A
; Patent No. 6828430
; GENERAL INFORMATION:
; APPLICANT: Rouleau, Guy A.
; APPLICANT: Brals, Bernard
; TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
; TITLE OF INVENTION: FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THEREOF
; FILE REFERENCE: 3028.1000-000
; CURRENT APPLICATION NUMBER: US/09/590,211A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: PCT/CA98/01133
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: 2,218,199
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-211A-4

Alignment Scores:
Pred. No.: 2.25e+04 Length: 30
Score: 46.00 Matches: 7

Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-590-211A-4 (1-30)

QY 139 ProProAlaArgProProProPro 147
DB 28 CCGCGCGCGCGCGCGCGCGCGCGCA 2

RESULT 34

US-09-828-034-7

; Sequence 7, Application US/09828034

; Patent No. 6967075

; GENERAL INFORMATION:

; APPLICANT: Zhong, Weidong

; APPLICANT: Hong, Zhi

; APPLICANT: Ferrari, Eric

; TITLE OF INVENTION: HCV REPLICASE COMPLEXES

; FILE REFERENCE: IN01165

; CURRENT APPLICATION NUMBER: US/09/828,034

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: U.S. 60/195,852

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 30

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA

US-09-828-034-7

Alignment Scores: Length: 30
Pred. No.: 2.25e+04 Matches: 7
Score: 46.00 Conservative: 0
Percent Similarity: 77.8% Mismatches: 2
Best Local Similarity: 77.8% Indels: 0
Query Match: 2.4% Gaps: 0
DB: 4

US-09-544-776-2 (1-373) x US-09-828-034-7 (1-30)

QY 139 ProProAlaArgProProProPro 147
DB 2 CCGCGCGCGCGCGCGCGCGCGCGCC 28

RESULT 35

US-08-014-943A-7/c

; Sequence 7, Application US/08014943A

; Patent No. 5545551

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: Cloning And Expression Of Pur Protein

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/014,943A

; FILING DATE: 02/FEB/1992

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-014-943A-7
Alignment Scores: Length: 24
Pred. No.: 1.97e+04 Matches: 8
Score: 45.00 Conservative: 0
Percent Similarity: 80.0% Mismatches: 0
Best Local Similarity: 80.0% Indels: 2
Query Match: 2.4% Gaps: 1
DB: 2

US-09-544-776-2 (1-373) x US-08-014-943A-7 (1-24)

QY 139 ProProAlaArgProProProPro 148
DB 24 CCCCC-----CCCCCCCCCCCCCCCC 1

RESULT 36

US-08-486-421-49/c

; Sequence 49, Application US/08486421

; Patent No. 5672479

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,421

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/470,911

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 6923-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-486-421-49

Alignment Scores:
Pred. No.: 1.97e+04 Length: 24
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x US-08-486-421-49 (1-24)
QY 139 ProProAlaArgProProProPro 148
DB 24 CCCCCC-----CCCCCCCCCCCCCCCCCCCC 1

RESULT 37
US-08-470-911-49/c
; Sequence 49, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-470-911-49

Alignment Scores:
Pred. No.: 1.97e+04 Length: 24
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x US-08-470-911-49 (1-24)
QY 139 ProProAlaArgProProProPro 148
DB 24 CCCCCC-----CCCCCCCCCCCCCCCCCCCC 1

RESULT 39
US-08-374-144-3/c
; Sequence 3, Application US/08374144
; Patent No. 5629147
; GENERAL INFORMATION:
; APPLICANT: Arogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; TITLE OF INVENTION: Maternal Blood For In Situ Hybridization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman Wilf & Fried
; STREET: 20 West Third Street, P.O. Box 703
; CITY: Media
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08053-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-470-911-49

Alignment Scores:
Pred. No.: 1.97e+04 Length: 24
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x US-08-470-911-49 (1-24)
QY 139 ProProAlaArgProProProPro 148
DB 24 CCCCCC-----CCCCCCCCCCCCCCCCCCCC 1
```

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; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,144
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-085
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-374-144-3

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: Gaps: 1

US-09-544-776-2 (1-373) x US-08-374-144-3 (1-25)
QY 139 ProProAlaArgProProProPro 148
Db 24 CCGCGG-----CCGCGCGCGCGCGCGCG 1

RESULT 40
US-08-775-164-3/c
; Sequence 3, Application US/08775164
; Patent No. 576843
; GENERAL INFORMATION:
; APPLICANT: Aptogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,164
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:
```

```
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-775-164-3

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: Gaps: 1

US-09-544-776-2 (1-373) x US-08-775-164-3 (1-25)
QY 139 ProProAlaArgProProProPro 148
Db 24 CCGCGG-----CCGCGCGCGCGCGCGCG 1

RESULT 41
US-08-775-609-3/c
; Sequence 3, Application US/08775609
; Patent No. 5858649
; GENERAL INFORMATION:
; APPLICANT: Aptogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-775-609-3

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Query Match: 2.4% Indels: 2
DB: Gaps: 1
```



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Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 1 Gaps: 1

US-09-544-776-2 (1-373) x US-08-775-609-3 (1-25)

Qy 139 ProProAlaArgProProProProPro 148
Db 24 CCGCGCG-----CCGCGCGCGCGCGCGCG 1

RESULT 42
US-08-775-607-3/c
; Sequence 3, Application US/08775607
; Patent No. 5861253
; GENERAL INFORMATION:
; APPLICANT: Arogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,607
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-775-607-3

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 1 Gaps: 1

US-09-544-776-2 (1-373) x US-08-775-607-3 (1-25)

Qy 139 ProProAlaArgProProProProPro 148
Db 24 CCGCGCG-----CCGCGCGCGCGCGCGCG 1

RESULT 43
US-08-976-427-26
; Sequence 26, Application US/08976427A
; Patent No. 6322968
; GENERAL INFORMATION:
; APPLICANT: Head, Steven R.
; APPLICANT: Golet, Philip
```

```
; APPLICANT: Karn, Jonathan
; APPLICANT: Boyce-Jacino, Michael
; TITLE OF INVENTION: De No. 63229680 or "Universal" Sequencing Array
; FILE REFERENCE: 04990.0049
; CURRENT APPLICATION NUMBER: US/08/976,427A
; CURRENT FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-976-427-26

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 1 Gaps: 1

US-09-544-776-2 (1-373) x US-08-976-427-26 (1-25)

Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCC-----CCCCCCCCCCCCCCCC 24

RESULT 44
US-09-648-312-26
; Sequence 26, Application US/09648312
; Patent No. 6337188
; GENERAL INFORMATION:
; APPLICANT: Head, Steven R.
; APPLICANT: Golet, Philip
; APPLICANT: Karn, Jonathan
; APPLICANT: Boyce-Jacino, Michael
; TITLE OF INVENTION: De No. 63371880 or "Universal" Sequencing Array
; FILE REFERENCE: 04990.0049
; CURRENT APPLICATION NUMBER: US/09/648,312
; CURRENT FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-09-648-312-26

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 1 Gaps: 1

US-09-544-776-2 (1-373) x US-09-648-312-26 (1-25)

Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCC-----CCCCCCCCCCCCCCCC 24

RESULT 45
US-09-896-650C-26
; Sequence 26, Application US/09896650C
; Patent No. 6946249
; GENERAL INFORMATION:
; APPLICANT: Head, Steven R.
```

; APPLICANT: COELET, Philip
; APPLICANT: KARN, Jonathan
; APPLICANT: BOYCE-JACINO, Michael
; TITLE OF INVENTION: De No. 6946249o or Universal Sequencing Array
; FILE REFERENCE: 13019-2
; CURRENT APPLICATION NUMBER: US/09/896,650C
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/976,427
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-896-650C-26

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x US-09-896-650C-26 (1-25)

QY 139 ProProAlaArgProProProPro 148
DB 1 CCCCCC-----CCGCCCGCGCGCGCGCGCG 24

RESULT 46

US93-06828-3/c
; Sequence 3, Application PC/TUS9306828
; GENERAL INFORMATION:
; APPLICANT: Asgari, Morteza
; APPLICANT: Bresser, Joel
; APPLICANT: Cubbage, Michael L
; APPLICANT: Praehad, Nagindra
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells In Maternal Blood For
; TITLE OF INVENTION: In Situ Hybridization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:
; STREET:
; CITY:
; STATE:
; COUNTRY:
; ZIP:

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk - 720 k
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06828
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-06828-3

Alignment Scores:
Pred. No.: 2.08e+04 Length: 25
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 7 Gaps: 1

US-09-544-776-2 (1-373) x PCT-US93-06828-3 (1-25)

QY 139 ProProAlaArgProProProPro 148
DB 24 CCGCGG-----CCGCCCGCGCGCGCGCGCG 1

RESULT 47

US-09-590-211A-3/c
; Sequence 3, Application US/09590211A
; Patent No. 6828430
; GENERAL INFORMATION:
; APPLICANT: Rouleau, Guy A.
; APPLICANT: Brais, Bernard
; TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
; TITLE OF INVENTION: FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THEREOF
; FILE REFERENCE: 3028.1000-000
; CURRENT APPLICATION NUMBER: US/09/590,211A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: PCT/CA98/01133
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: 2,218,199
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-211A-3

Alignment Scores:
Pred. No.: 2.3e+04 Length: 27
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 3 Gaps: 1

US-09-544-776-2 (1-373) x US-09-590-211A-3 (1-27)

QY 139 ProProAlaArgProProProPro 148
DB 25 CCGCGG-----CCGCCCGCGCGCGCGCGCGCA 2

RESULT 48

US-08-993-008A-2/c
; Sequence 2, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shioh-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder

```
/ STATE: CO
/ COUNTRY: US
/ ZIP: 80303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/993,008A
/ FILING DATE: 18-DEC-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/032,436
/ FILING DATE: 18-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sullivan, Sally A.
/ REGISTRATION NUMBER: 32,064
/ REFERENCE/DOCKET NUMBER: 33-95
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 303-499-8080
/ TELEFAX: 303-499-8089
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-993-008A-2

Alignment Scores:
Pred. No.: 2.4e+04 Length: 28
Score: 45.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-993-008A-2 (1-28)

Qy 143 ProProProProProLaSer 150
Db 27 CCTCCTCCCTCCACTCTCTCT 4

RESULT 49
US-08-993-008A-3
/ Sequence 3, Application US/08993008A
/ Patent No. 6153596
/ GENERAL INFORMATION:
/ APPLICANT: Liotta, Dennis C.
/ APPLICANT: Petros, John A.
/ APPLICANT: Wey, Shioh-Jyi
/ APPLICANT: Karr, Joan F.
/ APPLICANT: Pohl, Jan
/ TITLE OF INVENTION: Polycationic Oligomers
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Greenlee, Winner and Sullivan
/ STREET: 5370 Manhattan Circle, Suite 201
/ CITY: Boulder
/ STATE: CO
/ COUNTRY: US
/ ZIP: 80303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/993,008A
```

```
/ FILING DATE: 18-DEC-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/032,436
/ FILING DATE: 18-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sullivan, Sally A.
/ REGISTRATION NUMBER: 32,064
/ REFERENCE/DOCKET NUMBER: 33-95
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 303-499-8080
/ TELEFAX: 303-499-8089
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-993-008A-3

Alignment Scores:
Pred. No.: 2.4e+04 Length: 28
Score: 45.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-08-993-008A-3 (1-28)

Qy 143 ProProProProProLaSer 150
Db 2 CCTCCTCCCTCCACTCTCTCT 25

RESULT 50
US-08-068-747-4
/ Sequence 4, Application US/08068747
/ Patent No. 5695933
/ GENERAL INFORMATION:
/ APPLICANT: Schalling, Martin
/ APPLICANT: Hudson, Thomas J.
/ APPLICANT: Housman, David E.
/ TITLE OF INVENTION: Direct Determination of Expanded
/ NUCLEOTIDE REPEATS IN THE HUMAN GENOME
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
/ STREET: Two Militia Drive
/ CITY: Lexington
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/068,747
/ FILING DATE: 28-MAY-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: MIT-6141
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-4

Alignment Scores:
Pred. No.:      2.63e+04      Length:      30
Score:          45.00        Matches:      9
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:      0
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DB:               2          Gaps:           0

US-09-544-776-2 (1-373) x US-08-068-747-4 (1-30)

QY      34  GluGluGluGluGluGluGluGluGlu 42
Db       3  GAGGAGGAGGAGGAGGAGGAGGAGGAG 29

Search completed: October 21, 2006, 04:44:56
Job time : 246 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 21, 2006, 04:45:10 ; Search time 1484 Seconds
(without alignments)
4632.703 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLQSPVLVSSDSPPRPQ.....VRDAMAKIOAKTGLKRAE 373

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18932170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 2325740

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MTN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEADSIZE=500 -MINLEN=8 -MAXLEN=30 -HOST=abs04
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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53	2.8	30	6	US-10-057-467-12	Sequence 12, Appl
53	2.8	30	7	US-10-314-578-1096	Sequence 1096, Ap
53	2.8	30	8	US-10-433-899-9	Sequence 9, Appl
53	2.8	30	10	US-10-479-472A-5	Sequence 5, Appl
53	2.8	30	10	US-10-479-472A-6	Sequence 6, Appl
53	2.8	30	10	US-10-791-209A-6	Sequence 6, Appl
53	2.8	30	10	US-10-310-914A-171952	Sequence 171952,
51	2.7	24	11	US-10-310-914A-462664	Sequence 462664,
51	2.7	24	11	US-10-310-914A-1286261	Sequence 1286261,
51	2.7	25	11	US-10-310-914A-103505	Sequence 103505,
51	2.7	27	11	US-10-310-914A-1245216	Sequence 1245216,
50	2.6	24	11	US-10-310-914A-394516	Sequence 394516,
50	2.6	24	11	US-10-310-914A-1168845	Sequence 1168845,
50	2.6	26	11	US-10-310-914A-917680	Sequence 917680,
50	2.6	27	11	US-10-310-914A-394517	Sequence 394517,
50	2.6	28	9	US-10-455-453-27	Sequence 27, Appl
50	2.6	30	3	US-09-232-785-397	Sequence 397, App
50	2.6	30	6	US-10-101-487-1	Sequence 1, Appl
50	2.6	30	6	US-10-101-487-2	Sequence 2, Appl
50	2.6	30	6	US-10-101-487-63	Sequence 63, Appl
50	2.6	30	6	US-10-101-487-65	Sequence 65, Appl
50	2.6	30	10	US-10-939-988-1	Sequence 1, Appl
50	2.6	30	10	US-10-939-988-2	Sequence 2, Appl
50	2.6	30	10	US-10-939-988-63	Sequence 63, Appl
50	2.6	30	10	US-10-939-988-65	Sequence 65, Appl
50	2.6	30	11	US-10-310-914A-1168838	Sequence 1168838,
49	2.6	28	3	US-09-865-644-22	Sequence 22, Appl
48	2.5	24	11	US-10-310-914A-632084	Sequence 632084,
48	2.5	25	13	US-11-036-317-747520	Sequence 747520,
48	2.5	27	11	US-10-310-914A-187729	Sequence 187729,
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47	2.5	21	11	US-10-310-914A-1256722	Sequence 1256722,
47	2.5	22	11	US-10-310-914A-247833	Sequence 247833,
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47	2.5	22	11	US-10-310-914A-374796	Sequence 374796,
47	2.5	22	11	US-10-310-914A-427728	Sequence 427728,
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47	2.5	23	11	US-10-310-914A-717695	Sequence 717695,
47	2.5	23	11	US-10-310-914A-734524	Sequence 734524,
47	2.5	24	11	US-10-310-914A-138910	Sequence 138910,
47	2.5	24	11	US-10-310-914A-247848	Sequence 247848,
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47	2.5	24	11	US-10-310-914A-1310951	Sequence 1310951,
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47	2.5	24	11	US-10-310-914A-1323390	Sequence 1323390,
47	2.5	25	8	US-10-717-597-4352	Sequence 4352, Ap
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47	2.5	25	11	US-10-310-914A-139794	Sequence 139794,
47	2.5	25	11	US-10-310-914A-629645	Sequence 629645,
47	2.5	25	11	US-10-310-914A-938140	Sequence 938140,
47	2.5	25	11	US-10-310-914A-993470	Sequence 993470,
47	2.5	25	11	US-10-310-914A-1019983	Sequence 1019983,
47	2.5	25	11	US-10-310-914A-1215682	Sequence 1215682,
47	2.5	25	11	US-10-310-914A-1287825	Sequence 1287825,
47	2.5	25	13	US-11-036-317-961012	Sequence 261012,
47	2.5	25	13	US-11-036-317-312839	Sequence 312839,
47	2.5	25	13	US-11-036-317-822117	Sequence 822117,
47	2.5	25	13	US-11-036-317-834846	Sequence 834846,
47	2.5	25	13	US-11-036-317-876421	Sequence 876421,
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DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x US-10-479-472A-5 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 1 CCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30

RESULT 6

US-10-479-472A-6/c

; Sequence 6, Application US/10479472A

; Publication No. US20050118581A1

; GENERAL INFORMATION:

; APPLICANT: DEL-FAVERO, JURGEN PETER LODE

; APPLICANT: VAN BROECKHOVEN, CHRISTINE

; TITLE OF INVENTION: NOVEL BRAIN EXPRESSED GENE AND PROTEIN ASSOCIATED WITH

; TITLE OF INVENTION: BIPOLAR DISORDER

; FILE REFERENCE: JAB-1711

; CURRENT APPLICATION NUMBER: US/10/479,472A

; CURRENT FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: PCT/EP02/06316

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: EP 01202214.1

; PRIOR FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 6

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Illustrative

; OTHER INFORMATION: oligonucleotide

US-10-479-472A-6

Alignment Scores:

Pred. No.: 1.34e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x US-10-479-472A-6 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 30 CCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1

RESULT 7

US-10-791-209A-6/c

; Sequence 6, Application US/10791209A

; Publication No. US20050191636A1

; GENERAL INFORMATION:

; APPLICANT: Hahn, Soonkap

; TITLE OF INVENTION: DETECTION OF STRP, SUCH AS FRAGILE X SYNDROME

; FILE REFERENCE: 81671

; CURRENT APPLICATION NUMBER: US/10/791,209A

; CURRENT FILING DATE: 2004-03-01

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Synthetic Probe

US-10-791-209A-6

Alignment Scores:

Pred. No.: 1.34e+04 Length: 30
Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x US-10-791-209A-6 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 30 CCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1

RESULT 8

US-10-310-914A-171952/c

; Sequence 171952, Application US/10310914A

; Publication No. US2006000322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 171952

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-171952

Alignment Scores:

Pred. No.: 1.51e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-171952 (1-24)

QY 139 ProProAlaArgProProProPro 146

DB 24 CCACCTGCGCGCCACCACCGCCCT 1

RESULT 9

US-10-310-914A-462664

; Sequence 462664, Application US/10310914A

; Publication No. US2006000322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 462664

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-462664

Alignment Scores:

Pred. No.: 1.51e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-462664 (1-24)

QY 139 ProProAlaArgProProPro 146
Db 1 CCUCCGCGCAGGCCCGCGCCGCC 24

RESULT 10

US-10-310-914A-1286261
; Sequence 1286261, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286261
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1286261

Alignment Scores:
Pred. No.: 1.51e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1286261 (1-24)

QY 141 AlaArgProProProProPro 148
Db 1 GCUGGCGCCUCCUCCUCCUCCA 24

RESULT 11

US-10-310-914A-103505
; Sequence 103505, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 103505
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-103505

Alignment Scores:
Pred. No.: 1.6e+04 Length: 25
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-103505 (1-25)

QY 140 ProAlaArgProProProPro 147
Db 2 CCUGCAGCGCCUCCACGCCGCC 25

RESULT 12

US-10-310-914A-1245216
; Sequence 1245216, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1245216
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1245216

Alignment Scores:
Pred. No.: 1.77e+04 Length: 27
Score: 51.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.7% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1245216 (1-27)

QY 139 ProProAlaArgProProPro 147
Db 1 CCGCGCGCGCGCGCGCGCGCGCG 27

RESULT 13

US-10-310-914A-394516/c
; Sequence 394516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394516
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-394516

Alignment Scores:
Pred. No.: 1.86e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-394516 (1-24)

QY 143 ProProProProProProAlaSer 150
Db 24 CCGCGCGCGCGCGCGCGCGCATCT 1

RESULT 14

US-10-310-914A-1168845/c
; Sequence 1168845, Application US/10310914A
; Publication No. US20060003322A1

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; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1168845
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1168845

Alignment Scores:
Pred. No.:          Length: 24
Score:              1.86e+04
Matches:            50.00
Conservative:       100.0%
Best Local Similarity: 100.0%
Mismatch:           2.6%
Indels:             11
Gaps:               0
DB:

US-09-544-776-2 (1-373) x US-10-310-914A-1168845 (1-24)

QY      143 ProProProProProProLaSer 150
DB      24 CCGCGCGCGCGCGCGCGCTTCC 1

RESULT 15
US-10-310-914A-917680/c
; Sequence 917680, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 917680
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-917680

Alignment Scores:
Pred. No.:          Length: 26
Score:              2.07e+04
Matches:            50.00
Conservative:       100.0%
Best Local Similarity: 100.0%
Mismatch:           2.6%
Indels:             11
Gaps:               0
DB:

US-09-544-776-2 (1-373) x US-10-310-914A-917680 (1-26)

QY      143 ProProProProProProLaSer 150
DB      26 CCGCGCGCGCGCGCGCGCTGT 3

RESULT 16
US-10-310-914A-394517/c
; Sequence 394517, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
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; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394517
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-394517

Alignment Scores:
Pred. No.:          Length: 27
Score:              2.17e+04
Matches:            50.00
Conservative:       100.0%
Best Local Similarity: 100.0%
Mismatch:           2.6%
Indels:             11
Gaps:               0
DB:

US-09-544-776-2 (1-373) x US-10-310-914A-394517 (1-27)

QY      143 ProProProProProProLaSer 150
DB      24 CCGCGCGCGCGCGCGCATCT 1

RESULT 17
US-10-455-453-27/c
; Sequence 27, Application US/10455453
; Publication No. US20050010028A1
; GENERAL INFORMATION:
; APPLICANT: YANAGAWA, Hiroshi
; APPLICANT: DOI, Nobuhide
; APPLICANT: MIYAMOTO, Etsuko
; APPLICANT: TAKASHIMA, Hideaki
; APPLICANT: OYAMA, Rieko
; TITLE OF INVENTION: C-Terminal Modified Protein and Method for Producing the Same,
; TITLE OF INVENTION: Modifying Agent and Translation Template Used for Producing
; TITLE OF INVENTION: C-Terminal Modified Protein, and Method for Detecting Protein
; TITLE OF INVENTION: Interaction with Use of C-Terminal Modified Protein
; FILE REFERENCE: 2003-0781A/WMC/01416
; CURRENT APPLICATION NUMBER: US/10/455,453
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: JP 2000-373105
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 27
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer containing part
; OTHER INFORMATION: of c-jun and 8-repeated His-tags
US-10-455-453-27

Alignment Scores:
Pred. No.:          Length: 28
Score:              2.28e+04
Matches:            50.00
Conservative:       100.0%
Best Local Similarity: 81.8%
Mismatch:           2.6%
Indels:             9
Gaps:               1
DB:

US-09-544-776-2 (1-373) x US-10-455-453-27 (1-28)

QY      138 GluProProAlaArgProProProPro 148
DB      28 GAACCAACCA-----CCACCACCACCACCA 2

RESULT 18
US-09-232-785-397/c
; Sequence 397, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
```

APPLICANT: International Paper Co.
APPLICANT: Echt, Craig. S
APPLICANT: Nelson, C. Dana
TITLE OF INVENTION: MICROSAATELITE DNA MARKERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 4481/1E188US1
CURRENT APPLICATION NUMBER: US/09/232,785
CURRENT FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 09/232,884
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 397
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 30
TYPE: DNA
ORGANISM: Pinus taeda L.
US-09-232-785-397

Alignment Scores:
Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-232-785-397 (1-30)

QY 34 GluGluGluGluGluGluGluGluGlu 43

Db 30 GAAGAAGAAGAGAGAGAGAGAGAGAGAGAA 1

RESULT 19

US-10-101-487-1

Sequence 1, Application US/10101487
Publication No. US20020169125A1
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-10-101-487-1

Alignment Scores:
Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-101-487-1 (1-30)

QY 34 GluGluGluGluGluGluGluGluGlu 43

|||||

Db 1 GAAGAAGAAGAGAGAGAGAGAGAGAGAGAG 30

RESULT 20

US-10-101-487-2/c

Sequence 2, Application US/10101487
Publication No. US20020169125A1
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-10-101-487-2

Alignment Scores:

Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-101-487-2 (1-30)

QY 34 GluGluGluGluGluGluGluGluGlu 43

|||||

Db 30 GAGAAGAAGAGAGAGAGAGAGAGAGAGAA 1

RESULT 21

US-10-101-487-63

Sequence 63, Application US/10101487
Publication No. US20020169125A1
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
APPLICANT: PIETZ, GREGORY E.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-10-101-487-1

RESULT 25
US-10-939-988-63
; Sequence 63, Application US/10939988
; Publication No. US20050118136A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/939,988
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(30)
US-10-939-988-63
Alignment Scores:
Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 1 Gaps: 0
US-09-544-776-2 (1-373) x US-10-939-988-63 (1-30)
Qy 34 GluGluGluGluGluGluGluGlu 43
Db 1 GAAGAGAGAGAGAGAGAGAGAGAGAG 30
RESULT 26
US-10-939-988-65/c
; Sequence 65, Application US/10939988
; Publication No. US20050118136A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/939,988
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide
US-10-939-988-65
Alignment Scores:
Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 1 Gaps: 0
US-09-544-776-2 (1-373) x US-10-939-988-65 (1-30)
Qy 34 GluGluGluGluGluGluGluGlu 43
Db 30 GAGGAAGAAGAGAGAGAGAGAGAGAA 1
RESULT 27
US-10-310-914A-1168838/c
; Sequence 1168838, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1168838
; LENGTH: 30
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1168838
Alignment Scores:
Pred. No.: 2.5e+04 Length: 30
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x US-10-310-914A-1168838 (1-30)
Qy 143 ProProProProProAlaser 150
Db 26 CCGCGCGCGCGCGCGCGCTTC 3
RESULT 28
US-09-865-644-22/c
; Sequence 22, Application US/09865644
; Patent No. US20020045188A1
; GENERAL INFORMATION:
; APPLICANT: Kamb et al
; TITLE OF INVENTION: METHODS FOR VALIDATING POLYPEPTIDE TARGETS THAT CORRELATE TO
; FILE REFERENCE: 29345/37561
; CURRENT APPLICATION NUMBER: US/09/865,644
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: DNA
; ORGANISM: OVT 1561
US-09-865-644-22
Alignment Scores:
Pred. No.: 2.8e+04 Length: 28
Score: 49.00 Matches: 7

Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 77.8% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x US-09-865-644-22 (1-28)

QY 142 ArgProProProProProProPro 150
DB 27 CGCCCCCGCGCGCCCTTCCTCCGCC 1

RESULT 29

US-10-310-914A-632084
; Sequence 632084, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Shiler, Kvuzat
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 632084
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-632084

Alignment Scores:
Pred. No.: 2.81e+04 Length: 24
Score: 48.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-632084 (1-24)

QY 141 AlaArgProProProProProPro 148
DB 1 UCCCGCGCGCGCGCCGCGCG 24

RESULT 30

US-11-036-317-747520
; Sequence 747520, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 747520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-747520

Alignment Scores:
Pred. No.: 2.97e+04 Length: 25
Score: 48.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 13 Gaps: 0

US-09-544-776-2 (1-373) x US-11-036-317-747520 (1-25)
QY 191 TyrTrpArgAspIleLysLysThr 198
DB 1 TACTGGAGAGACATTAAAGAGACT 24

RESULT 31

US-10-310-914A-187729/c
; Sequence 187729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 187729
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-187729

Alignment Scores:
Pred. No.: 3.29e+04 Length: 27
Score: 48.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-187729 (1-27)

QY 140 ProAlaArgProProProProPro 148
DB 27 CCTCCACCCCTCCTCCGCGCCCT 1

RESULT 32

US-10-310-914A-1119929/c
; Sequence 1119929, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1119929
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1119929

Alignment Scores:
Pred. No.: 2.9e+04 Length: 21
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0
US-09-544-776-2 (1-373) x US-10-310-914A-1119929 (1-21)
QY 142 ArgProProProProProPro 148
DB: |||||

```
Db      21  CGGCCGCCACCAACCCGCCCT 1
RESULT 33
US-10-310-914A-1256722
; Sequence 1256722, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1256722
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1256722
Alignment Scores:
Pred. No.:      2.9e+04      Length:      21
Score:          47.00      Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    2.5%      Indels:      0
DB:             11      Gaps:      0
US-09-544-776-2 (1-373) x US-10-310-914A-1256722 (1-21)

QY      142  ArgProProProProPro 148
Db      1  CGGCCGCCGCCGCCGCCGCC 21
RESULT 34
US-10-310-914A-247833/c
; Sequence 247833, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 247833
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-247833
Alignment Scores:
Pred. No.:      3.08e+04      Length:      22
Score:          47.00      Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    2.5%      Indels:      0
DB:             11      Gaps:      0
US-09-544-776-2 (1-373) x US-10-310-914A-247833 (1-22)

QY      142  ArgProProProProPro 148
Db      22  CGCCCCCGCCCTCCGCCGCCA 2
RESULT 35
US-10-310-914A-349189
; Sequence 349189, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 349189
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-349189
Alignment Scores:
Pred. No.:      3.08e+04      Length:      22
Score:          47.00      Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    2.5%      Indels:      0
DB:             11      Gaps:      0
US-09-544-776-2 (1-373) x US-10-310-914A-349189 (1-22)

QY      142  ArgProProProProPro 148
Db      2  CGGCCGCCGCCGCCGCCCCU 22
RESULT 36
US-10-310-914A-374796
; Sequence 374796, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 374796
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-374796
Alignment Scores:
Pred. No.:      3.08e+04      Length:      22
Score:          47.00      Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    2.5%      Indels:      0
DB:             11      Gaps:      0
US-09-544-776-2 (1-373) x US-10-310-914A-374796 (1-22)

QY      142  ArgProProProProPro 148
Db      2  CGGCCGCCGCCGCCGCCCCU 22
RESULT 37
US-10-310-914A-427728
; Sequence 427728, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
```

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; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 427728
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-427728

Alignment Scores:
Pred. No.:      3.08e+04      Length:      22
Score:          47.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.5%         Indels:      0
DB:             11          Gaps:      0

US-09-544-776-2 (1-373) x US-10-310-914A-427728 (1-22)

QY      142 ArgProProProProPro 148
Db      1 CGGCCUCCCGCCGCCCCCA 21

RESULT 38
US-10-310-914A-430430
; Sequence 430430, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 430430
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-430430

Alignment Scores:
Pred. No.:      3.08e+04      Length:      22
Score:          47.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.5%         Indels:      0
DB:             11          Gaps:      0

US-09-544-776-2 (1-373) x US-10-310-914A-430430 (1-22)

QY      142 ArgProProProProPro 148
Db      1 CGGCCUCCCGCCGCCCCCA 21

RESULT 39
US-10-310-914A-400367
; Sequence 400367, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 400367
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-400367

Alignment Scores:
Pred. No.:      3.27e+04      Length:      23
Score:          47.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.5%         Indels:      0
DB:             11          Gaps:      0

US-09-544-776-2 (1-373) x US-10-310-914A-400367 (1-23)

QY      142 ArgProProProProPro 148
Db      1 CGGCCUCCCGCCGCCCCCA 21

RESULT 40
US-10-310-914A-427716
; Sequence 427716, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 427716
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-427716

Alignment Scores:
Pred. No.:      3.27e+04      Length:      23
Score:          47.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.5%         Indels:      0
DB:             11          Gaps:      0

US-09-544-776-2 (1-373) x US-10-310-914A-427716 (1-23)

QY      142 ArgProProProProPro 148
Db      3 CGGCCUCCCGCCGCCCCCA 23

RESULT 41
US-10-310-914A-624948/c
; Sequence 624948, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 624948
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
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US-10-310-914A-624948

Alignment Scores: 3.27e+04 Length: 23
Pred. No.: 47.00 Matches: 7
Score: 47.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-624948 (1-23)

QY 142 ArgProProProProPro 148

DB 22 AGCGCCACCAACCACCA 2

RESULT 42

US-10-310-914A-717695/c
; Sequence 717695, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 717695
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-717695

Alignment Scores: 3.27e+04 Length: 23
Pred. No.: 47.00 Matches: 7
Score: 47.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-717695 (1-23)

QY 142 ArgProProProProPro 148

DB 21 CGACCCCAACCACCCCA 1

RESULT 43

US-10-310-914A-734524
; Sequence 734524, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 734524
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-734524

Alignment Scores: 3.27e+04 Length: 23
Pred. No.: 47.00 Matches: 7
Score: 47.00

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-734524 (1-23)

QY 142 ArgProProProProPro 148

DB 3 CGCGCCCGCCGCCGCCG 23

RESULT 44

US-10-310-914A-138910/c
; Sequence 138910, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138910
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-138910

Alignment Scores: 3.46e+04 Length: 24
Pred. No.: 47.00 Matches: 7
Score: 47.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-138910 (1-24)

QY 142 ArgProProProProPro 148

DB 21 CGCGCCCGCCGCCGCCCT 1

RESULT 45

US-10-310-914A-247848/c
; Sequence 247848, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 247848
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-247848

Alignment Scores: 3.46e+04 Length: 24
Pred. No.: 47.00 Matches: 7
Score: 47.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-247848 (1-24)

QY 142 ArgProProProProPro 148
DB 24 CGGCCCTCCGCCCGCCG 4

RESULT 46

US-10-310-914A-406855
; Sequence 406855, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 406855
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-406855

Alignment Scores:
Pred. No.: 3.46e+04 Length: 24
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-406855 (1-24)

QY 143 ProProProProProAlaser 150
DB 1 CCUCCUCCUCCUCCUCCUCCU 24

RESULT 47

US-10-310-914A-427729
; Sequence 427729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 427729
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-427729

Alignment Scores:
Pred. No.: 3.46e+04 Length: 24
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-427729 (1-24)

QY 142 ArgProProProProPro 148
DB 1 CGGCCUCCUCCUCCUCCUCCU 21

RESULT 48

US-10-310-914A-1310951
; Sequence 1310951, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1310951
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1310951

Alignment Scores:
Pred. No.: 3.46e+04 Length: 24
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1310951 (1-24)

QY 142 ArgProProProProPro 148
DB 4 CGCCCGCCGCCGCCGCCG 24

RESULT 49

US-10-310-914A-1310952
; Sequence 1310952, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1310952
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1310952

Alignment Scores:
Pred. No.: 3.46e+04 Length: 24
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 11 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1310952 (1-24)

QY 142 ArgProProProProPro 148
DB 4 CGCCCGCCGCCGCCGCCG 24

RESULT 50

US-10-310-914A-1323390
; Sequence 1323390, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1323390
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1323390

Alignment Scores: Length: 24
Pred. No.: 3.46e+04 Matches: 7
Score: 47.00 Conservative: 1
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 87.5% Indels: 0
Query Match: 2.5% Gaps: 0
DB: 11

US-09-544-776-2 (1-373) x US-10-310-914A-1323390 (1-24)

QY 140 ProAlaArgProProProPro 147
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Db 1 CCUGCCCAACCCCGCCCGCC 24

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Listing first 150 summaries

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 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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SUMMARIES

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2	45	2.4	24	9	US-11-339-222-428 Sequence 428, App
3	45	2.4	24	9	US-11-339-222-963 Sequence 963, App
4	45	2.4	27	7	US-11-339-222-915 Sequence 915, App
5	43	2.3	21	7	US-11-339-222-941 Sequence 941, App
6	43	2.3	21	7	US-11-339-222-977 Sequence 977, App
7	43	2.3	23	7	US-11-339-222-667 Sequence 667, App

23	2.3	43	8	7	US-11-339-222-670	Sequence 670, App
23	2.3	43	9	7	US-11-339-222-673	Sequence 673, App
23	2.3	43	10	7	US-11-339-222-676	Sequence 676, App
23	2.3	43	11	7	US-11-339-222-678	Sequence 678, App
23	2.3	43	12	7	US-11-339-222-937	Sequence 937, App
23	2.3	43	13	7	US-11-339-222-940	Sequence 940, App
23	2.3	43	14	7	US-11-339-222-942	Sequence 942, App
23	2.3	43	15	7	US-11-339-222-943	Sequence 943, App
23	2.3	43	16	7	US-11-339-222-946	Sequence 946, App
23	2.3	43	17	7	US-11-339-222-948	Sequence 948, App
23	2.3	43	18	7	US-11-339-222-949	Sequence 949, App
23	2.3	43	19	7	US-11-339-222-952	Sequence 952, App
23	2.3	43	20	7	US-11-339-222-954	Sequence 954, App
23	2.3	43	21	7	US-11-339-222-973	Sequence 973, App
23	2.3	43	22	7	US-11-339-222-976	Sequence 976, App
23	2.3	43	23	7	US-11-339-222-978	Sequence 978, App
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23	2.3	43	25	7	US-11-339-222-982	Sequence 982, App
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23	2.3	43	28	6	US-10-858-164-990	Sequence 990, App
23	2.3	43	29	6	US-10-858-164-990	Sequence 990, App
23	2.3	43	30	6	US-10-858-013-989	Sequence 989, App
23	2.3	43	31	6	US-10-858-164-989	Sequence 989, App
23	2.3	43	32	6	US-10-668-050-133	Sequence 133, App
23	2.3	43	33	6	US-10-858-146-989	Sequence 989, App
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23	2.3	43	35	8	US-11-254-920-12	Sequence 12, Appl
23	2.3	43	36	8	US-11-254-920-13	Sequence 13, Appl
23	2.3	43	37	9	US-11-301-360-243	Sequence 243, App
23	2.3	43	38	9	US-11-301-360-257	Sequence 257, App
23	2.3	43	39	9	US-11-301-360-530	Sequence 530, App
23	2.3	43	40	9	US-11-301-360-531	Sequence 531, App
23	2.3	43	41	9	US-11-301-360-811	Sequence 811, App
23	2.3	43	42	9	US-11-301-360-987	Sequence 987, App
23	2.3	43	43	7	US-11-339-222-920	Sequence 920, App
23	2.3	43	44	7	US-11-339-222-931	Sequence 931, App
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23	2.3	43	46	7	US-11-339-222-936	Sequence 936, App
23	2.3	43	47	7	US-11-339-222-936	Sequence 936, App
23	2.3	43	48	8	US-11-255-691-31	Sequence 31, Appl
23	2.3	43	49	6	US-10-858-013-987	Sequence 987, App
23	2.3	43	50	6	US-10-858-164-987	Sequence 987, App
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23	2.3	43	58	6	US-10-858-164-985	Sequence 985, App
23	2.3	43	59	6	US-11-301-554-1915	Sequence 1915, App
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23	2.3	43	78	6	US-11-339-222-679	Sequence 679, App
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92	41	2.1	23	7	US-11-339-222-912	Sequence 912, App
93	41	2.1	23	7	US-11-339-222-913	Sequence 913, App
94	41	2.1	23	7	US-11-339-222-916	Sequence 916, App
95	41	2.1	23	7	US-11-339-222-918	Sequence 918, App
96	41	2.1	23	7	US-11-339-222-955	Sequence 955, App
97	41	2.1	23	7	US-11-339-222-958	Sequence 958, App
98	41	2.1	23	7	US-11-339-222-960	Sequence 960, App
99	41	2.1	23	7	US-11-339-222-961	Sequence 961, App
100	41	2.1	23	7	US-11-339-222-964	Sequence 964, App
101	41	2.1	23	7	US-11-339-222-966	Sequence 966, App
102	41	2.1	23	7	US-11-339-222-967	Sequence 967, App
103	41	2.1	23	7	US-11-339-222-970	Sequence 970, App
104	41	2.1	23	7	US-11-339-222-972	Sequence 972, App
105	41	2.1	25	9	US-11-348-413-216505	Sequence 216505,
106	41	2.1	25	9	US-11-348-413-216506	Sequence 216506,
107	40	2.1	23	7	US-11-339-222-1099	Sequence 1099, Ap
108	40	2.1	23	7	US-11-339-222-1102	Sequence 1102, Ap
109	40	2.1	23	7	US-11-339-222-1105	Sequence 1105, Ap
110	40	2.1	23	7	US-11-339-222-1108	Sequence 1108, Ap
111	40	2.1	23	7	US-11-339-222-1110	Sequence 1110, Ap
112	40	2.1	25	9	US-11-348-413-216508	Sequence 216508,
113	40	2.1	25	9	US-11-348-413-216509	Sequence 216509,
114	40	2.1	25	9	US-11-348-413-671809	Sequence 671809,
115	40	2.1	25	9	US-11-348-413-671810	Sequence 671810,
116	40	2.1	28	6	US-10-511-436A-19	Sequence 19, Appl
117	40	2.1	30	7	US-11-404-939-72	Sequence 72, Appl
118	39	2.0	21	7	US-11-339-222-887	Sequence 887, App
119	39	2.0	21	7	US-11-339-222-974	Sequence 974, App
120	39	2.0	21	7	US-11-339-222-1079	Sequence 1079, Ap
121	39	2.0	21	7	US-11-339-222-1089	Sequence 1089, Ap
122	39	2.0	21	7	US-11-339-222-1112	Sequence 1112, Ap
123	39	2.0	21	7	US-11-339-222-1115	Sequence 1115, Ap
124	39	2.0	21	7	US-11-339-222-1133	Sequence 1133, Ap
125	39	2.0	23	6	US-10-858-013-935	Sequence 935, App
126	39	2.0	23	6	US-10-858-164-935	Sequence 935, App
127	39	2.0	23	6	US-10-858-164-935	Sequence 935, App
128	39	2.0	23	7	US-11-339-222-883	Sequence 883, App
129	39	2.0	23	7	US-11-339-222-886	Sequence 886, App
130	39	2.0	23	7	US-11-339-222-888	Sequence 888, App
131	39	2.0	23	7	US-11-339-222-889	Sequence 889, App
132	39	2.0	23	7	US-11-339-222-892	Sequence 892, App
133	39	2.0	23	7	US-11-339-222-894	Sequence 894, App
134	39	2.0	23	7	US-11-339-222-895	Sequence 895, App
135	39	2.0	23	7	US-11-339-222-898	Sequence 898, App
136	39	2.0	23	7	US-11-339-222-900	Sequence 900, App
137	39	2.0	23	7	US-11-339-222-1075	Sequence 1075, Ap
138	39	2.0	23	7	US-11-339-222-1078	Sequence 1078, Ap
139	39	2.0	23	7	US-11-339-222-1080	Sequence 1080, Ap
140	39	2.0	23	7	US-11-339-222-1081	Sequence 1081, Ap
141	39	2.0	23	7	US-11-339-222-1084	Sequence 1084, Ap
142	39	2.0	23	7	US-11-339-222-1086	Sequence 1086, Ap
143	39	2.0	23	7	US-11-339-222-1087	Sequence 1087, Ap
144	39	2.0	23	7	US-11-339-222-1090	Sequence 1090, Ap
145	39	2.0	23	7	US-11-339-222-1092	Sequence 1092, Ap
146	39	2.0	23	7	US-11-339-222-1111	Sequence 1111, Ap
147	39	2.0	23	7	US-11-339-222-1114	Sequence 1114, Ap
148	39	2.0	23	7	US-11-339-222-1116	Sequence 1116, Ap
149	39	2.0	23	7	US-11-339-222-1117	Sequence 1117, Ap
150	39	2.0	23	7	US-11-339-222-1120	Sequence 1120, Ap

ALIGNMENTS

RESULT 1		US-11-301-360-770		Sequence 685, App	
				Sequence 688, App	
				Sequence 690, App	
				Sequence 691, App	
				Sequence 694, App	
				Sequence 901, App	
				Sequence 904, App	
				Sequence 906, App	
				Sequence 910, App	
				Sequence 912, App	
				Sequence 913, App	
				Sequence 916, App	
				Sequence 918, App	
				Sequence 955, App	
				Sequence 958, App	
				Sequence 960, App	
				Sequence 961, App	
				Sequence 964, App	
				Sequence 966, App	
				Sequence 967, App	
				Sequence 970, App	
				Sequence 972, App	
				Sequence 216505,	
				Sequence 216506,	
				Sequence 1099, Ap	
				Sequence 1102, Ap	
				Sequence 1105, Ap	
				Sequence 1108, Ap	
				Sequence 1110, Ap	
				Sequence 216508,	
				Sequence 216509,	
				Sequence 671809,	
				Sequence 671810,	
				Sequence 19, Appl	
				Sequence 72, Appl	
				Sequence 887, App	
				Sequence 974, App	
				Sequence 1079, Ap	
				Sequence 1089, Ap	
				Sequence 1112, Ap	
				Sequence 1115, Ap	
				Sequence 1133, Ap	
				Sequence 935, App	
				Sequence 935, App	
				Sequence 883, App	
				Sequence 886, App	
				Sequence 888, App	
				Sequence 892, App	
				Sequence 894, App	
				Sequence 895, App	
				Sequence 898, App	
				Sequence 900, App	
				Sequence 1075, Ap	
				Sequence 1078, Ap	
				Sequence 1080, Ap	
				Sequence 1081, Ap	
				Sequence 1084, Ap	
				Sequence 1086, Ap	
				Sequence 1087, Ap	
				Sequence 1090, Ap	
				Sequence 1092, Ap	
				Sequence 1111, Ap	
				Sequence 1114, Ap	
				Sequence 1116, Ap	
				Sequence 1117, Ap	
				Sequence 1120, Ap	

Alignment Scores: 1.07e+05 Length: 28
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-770 (1-28)

Qy 139 ProProlaArgProProProProPro 147
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 2

US-11-301-360-428		Sequence 428, Application US/11301360	
		Publication No. US20060154890A1	
		GENERAL INFORMATION:	
		APPLICANT: Bratzler, Robert L.	
		APPLICANT: Petersen, Deanna M.	
		APPLICANT: Fouron, Yves	
		TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE	
		TREATMENT OF ASTHMA AND ALLERGY	
		FILE REFERENCE: C1037.70013US02	
		CURRENT APPLICATION NUMBER: US/11/301,360	
		CURRENT FILING DATE: 2005-12-03	
		PRIOR APPLICATION NUMBER: US 09/776,479	
		PRIOR FILING DATE: 2001-02-02	
		PRIOR APPLICATION NUMBER: US 60/179,991	
		PRIOR FILING DATE: 2000-02-03	
		NUMBER OF SEQ ID NOS: 1093	
		SOFTWARE: FastSeq for Windows Version 3.0	

```
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: Gaps: 1

US-09-544-776-2 (1-373) x US-11-301-360-428 (1-24)
QY 139 ProProAlaArgProProProPro 148
DB 1 CCCCCC-----CCCCCCCCCCCCCCCCCCCC 24

RESULT 3
US-11-301-360-963
; Sequence 963, Application US/11301360
; Publication No. US20060154890A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; TREATMENT OF ASTHMA AND ALLERGY
; FILE REFERENCE: C1037.70013US02
; CURRENT APPLICATION NUMBER: US/11/301,360
; PRIOR FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 963
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-301-360-963

Alignment Scores:
Pred. No.: 1.04e+05 Length: 24
Score: 45.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: Gaps: 1

US-09-544-776-2 (1-373) x US-11-301-360-963 (1-24)
QY 139 ProProAlaArgProProProPro 148
DB 1 CCCCCC-----CCCCCCCCCCCCCCCCCCCC 24

RESULT 4
US-11-390-810-13/c
; Sequence 13, Application US/11390810
; Publication No. US20060229303A1
; GENERAL INFORMATION:
; APPLICANT: WHITTEN, Jeffrey P.
; APPLICANT: SCHWABE, Michael
; APPLICANT: SIDDQUI-JAIN, Adam
; APPLICANT: MORAN, Terrance
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS
; FILE REFERENCE: 53232001110
; CURRENT APPLICATION NUMBER: US/11/390,810
; CURRENT FILING DATE: 2006-03-28
; PRIOR APPLICATION NUMBER: US 10/821,243
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/461,271
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/463,171
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/519,535
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/532,727
```

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; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-390-810-13

Alignment Scores:
Pred. No.: 1.15e+05 Length: 27
Score: 45.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-11-390-810-13 (1-27)
QY 143 ProProProProProAlaSer 150
DB 27 CCTCTCTCTCCACCTCCTCTCT 4

RESULT 5
US-11-339-222-941
; Sequence 941, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 941
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = guanosine
US-11-339-222-941

Alignment Scores:
Pred. No.: 1.14e+05 Length: 21
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-941 (1-21)
QY 249 AspGluGlyHisProPheArg 255
DB 1 GAUGAAGGCCACCAUUCAGG 21

RESULT 6
US-11-339-222-977
; Sequence 977, Application US/11339222
; Publication No. US20060217324A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 977
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = guanosine
US-11-339-222-977

Alignment Scores:
Pred. No.: 1,14e+05 Length: 21
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-977 (1-21)
QY 251 GlyHisProPheArgAlaTyr 257
Db 1 GGCACCCCAUUCAGGCAUAU 21

RESULT 7
US-11-339-222-667
; Sequence 667, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 667
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
US-11-339-222-667

; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 667
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
US-11-339-222-667
```

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Alignment Scores:
Pred. No.: 1,24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-667 (1-23)
QY 191 TyrTrpArgAspIleLysLys 197
Db 3 UACUGGAGAGACAUUAGAAG 23

RESULT 8
US-11-339-222-670
; Sequence 670, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 670
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = guanosine
US-11-339-222-670

Alignment Scores:
Pred. No.: 1,24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-670 (1-23)
QY 191 TyrTrpArgAspIleLysLys 197
Db 2 UACUGGAGAGACAUUAGAAG 22

RESULT 9
US-11-339-222-673
; Sequence 673, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
```


;
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 673
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
; US-11-339-222-673

Alignment Scores:
Pred. No.: 1-24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-673 (1-23)

QY 191 TyTtpArgAspIleLysLys 197
Db 1 UACUGGAGAGACAUUAGAAG 21

RESULT 10

US-11-339-222-676
; Sequence 676, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 676
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
; US-11-339-222-676

Alignment Scores:
Pred. No.: 1-24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-676 (1-23)

QY 191 TyTtpArgAspIleLysLys 197
Db 1 UACUGGAGAGACAUUAGAAG 21

RESULT 11

US-11-339-222-678/c
; Sequence 678, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 678
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = guanosine
; US-11-339-222-678

Alignment Scores:
Pred. No.: 1-24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-678 (1-23)

QY 191 TyTtpArgAspIleLysLys 197
Db 23 TACTGGAGAGACATTAGAAG 3

RESULT 12

US-11-339-222-937
; Sequence 937, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624

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; SEQ ID NO 937
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = cytidine
US-11-339-222-937
Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0
US-09-544-776-2 (1-373) x US-11-339-222-937 (1-23)
Oy 249 AspGluGlyHisPropheArg 255
Db 3 GAUGAAGGCCCAUUCAGG 23
RESULT 13
US-11-339-222-940
; Sequence 940, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 940
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = cytidine
US-11-339-222-942
Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0
US-09-544-776-2 (1-373) x US-11-339-222-942 (1-23)
Oy 249 AspGluGlyHisPropheArg 255
Db 21 GATGAAGGCCCAUUCAGG 1
RESULT 15
US-11-339-222-943
; Sequence 943, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 943
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = cytidine
US-11-339-222-940
Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0
US-09-544-776-2 (1-373) x US-11-339-222-940 (1-23)
Oy 249 AspGluGlyHisPropheArg 255
Db 3 GAUGAAGGCCCAUUCAGG 23
RESULT 14
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LOCATION: 1
OTHER INFORMATION: /mod_base = adenosine
US-11-339-222-943

Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-943 (1-23)

QY 249 AspGluGlyHisProphearg 255

DB 2 GAUGAAGGCCACCAUUCAGG 22

RESULT 16

US-11-339-222-946
Sequence 946, Application US/11339222
Publication No. US20060217324A1
GENERAL INFORMATION:
APPLICANT: Soutschek, Juergen
TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
FILE REFERENCE: 14174-101001
CURRENT APPLICATION NUMBER: US/11/339,222
CURRENT FILING DATE: 2006-01-24
PRIOR APPLICATION NUMBER: US 60/646,353
PRIOR FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/701,470
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/726,838
PRIOR FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: US 60/748,316
PRIOR FILING DATE: 2005-12-07
NUMBER OF SEQ ID NOS: 1624
SEQ ID NO 946
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: siRNAs specific for Nogo-L
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base = adenosine
US-11-339-222-946

Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-946 (1-23)

QY 249 AspGluGlyHisProphearg 255

DB 2 GAUGAAGGCCACCAUUCAGG 22

RESULT 17

US-11-339-222-948/c
Sequence 948, Application US/11339222
Publication No. US20060217324A1
GENERAL INFORMATION:
APPLICANT: Soutschek, Juergen
TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
FILE REFERENCE: 14174-101001

CURRENT APPLICATION NUMBER: US/11/339,222
CURRENT FILING DATE: 2006-01-24
PRIOR APPLICATION NUMBER: US 60/646,353
PRIOR FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/701,470
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/726,838
PRIOR FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: US 60/748,316
PRIOR FILING DATE: 2005-12-07
NUMBER OF SEQ ID NOS: 1624
SEQ ID NO 948
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: siRNAs specific for Nogo-L
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base = cytidine
US-11-339-222-948

Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-948 (1-23)

QY 249 AspGluGlyHisProphearg 255

DB 22 GATGAAGGCCACCATTCAGG 2

RESULT 18

US-11-339-222-949
Sequence 949, Application US/11339222
Publication No. US20060217324A1
GENERAL INFORMATION:
APPLICANT: Soutschek, Juergen
TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
FILE REFERENCE: 14174-101001
CURRENT APPLICATION NUMBER: US/11/339,222
CURRENT FILING DATE: 2006-01-24
PRIOR APPLICATION NUMBER: US 60/646,353
PRIOR FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/701,470
PRIOR FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/726,838
PRIOR FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: US 60/748,316
PRIOR FILING DATE: 2005-12-07
NUMBER OF SEQ ID NOS: 1624
SEQ ID NO 949
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: siRNAs specific for Nogo-L
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base = guanosine
US-11-339-222-949

Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-949 (1-23)

Qy 249 AspGluGlyHisPropheArg 255
Db 1 GAUGAAGGCCCAUUCAGG 21

RESULT 19

US-11-339-222-952

; Sequence 952, Application US/11339222

; Publication No. US20060217324A1

; GENERAL INFORMATION:

; APPLICANT: Soutschek, Juergen

; APPLICANT: Vornlocher, Hans-Peter

; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF

; FILE REFERENCE: 14174-101001

; CURRENT APPLICATION NUMBER: US/11/339,222

; CURRENT FILING DATE: 2006-01-24

; PRIOR APPLICATION NUMBER: US 60/646,353

; PRIOR FILING DATE: 2005-01-24

; PRIOR APPLICATION NUMBER: US 60/701,470

; PRIOR FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/726,838

; PRIOR FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: US 60/748,316

; PRIOR FILING DATE: 2005-12-07

; NUMBER OF SEQ ID NOS: 1624

; SEQ ID NO 952

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: siRNAs specific for Nogo-L

; NAME/KEY: modified_base

; LOCATION: 1

; OTHER INFORMATION: /mod_base = guanosine

US-11-339-222-952

Alignment Scores:

Pred. No.: 1.24e+05 Length: 23

Score: 43.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 2.3% Indels: 0

DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-952 (1-23)

Qy 249 AspGluGlyHisPropheArg 255

Db 1 GAUGAAGGCCCAUUCAGG 21

RESULT 20

US-11-339-222-954/c

; Sequence 954, Application US/11339222

; Publication No. US20060217324A1

; GENERAL INFORMATION:

; APPLICANT: Soutschek, Juergen

; APPLICANT: Vornlocher, Hans-Peter

; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF

; FILE REFERENCE: 14174-101001

; CURRENT APPLICATION NUMBER: US/11/339,222

; CURRENT FILING DATE: 2006-01-24

; PRIOR APPLICATION NUMBER: US 60/646,353

; PRIOR FILING DATE: 2005-01-24

; PRIOR APPLICATION NUMBER: US 60/701,470

; PRIOR FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/726,838

; PRIOR FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 954

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: siRNAs specific for Nogo-L

; NAME/KEY: modified_base

; LOCATION: 1

; OTHER INFORMATION: /mod_base = guanosine

US-11-339-222-954

Alignment Scores:

Pred. No.: 1.24e+05 Length: 23

Score: 43.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 2.3% Indels: 0

DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-954 (1-23)

Qy 249 AspGluGlyHisPropheArg 255

Db 23 GATGAAGGCCCAUUCAGG 3

RESULT 21

US-11-339-222-973

; Sequence 973, Application US/11339222

; Publication No. US20060217324A1

; GENERAL INFORMATION:

; APPLICANT: Soutschek, Juergen

; APPLICANT: Vornlocher, Hans-Peter

; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF

; FILE REFERENCE: 14174-101001

; CURRENT APPLICATION NUMBER: US/11/339,222

; CURRENT FILING DATE: 2006-01-24

; PRIOR APPLICATION NUMBER: US 60/646,353

; PRIOR FILING DATE: 2005-01-24

; PRIOR APPLICATION NUMBER: US 60/701,470

; PRIOR FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/726,838

; PRIOR FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: US 60/748,316

; PRIOR FILING DATE: 2005-12-07

; NUMBER OF SEQ ID NOS: 1624

; SEQ ID NO 973

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: siRNAs specific for Nogo-L

; NAME/KEY: modified_base

; LOCATION: 1

; OTHER INFORMATION: /mod_base = adenosine

US-11-339-222-973

Alignment Scores:

Pred. No.: 1.24e+05 Length: 23

Score: 43.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 2.3% Indels: 0

DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-973 (1-23)

Qy 251 GlyHisPropheArgAlaTyr 257

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Db      3  GGGCACCACCAUUCAGGGCAUAAU 23
RESULT 22
US-11-339-222-976
; Sequence 976, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 976
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = adenosine
US-11-339-222-976
Alignment Scores:
Pred. No.:      1.24e+05      Length:      23
Score:          43.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.3%         Indels:       0
DB:             7           Gaps:         0
US-09-544-776-2 (1-373) x US-11-339-222-976 (1-23)
QY      251 GlyHisProPheArgAlaTyr 257
Db      21  GGGCACCACCAUUCAGGGCATAT 1
RESULT 24
US-11-339-222-979
; Sequence 979, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 979
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = adenosine
US-11-339-222-979
Alignment Scores:
Pred. No.:      1.24e+05      Length:      23
Score:          43.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    2.3%         Indels:       0
DB:             7           Gaps:         0
US-09-544-776-2 (1-373) x US-11-339-222-979 (1-23)
QY      251 GlyHisProPheArgAlaTyr 257
Db      2  GGGCACCACCAUUCAGGGCAUAAU 22
RESULT 25
US-11-339-222-982
; Sequence 982, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
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; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 982
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = guanosine
; US-11-339-222-982

Alignment Scores:
Pred. No.: 1.24e+05 Length: 23
Score: 43.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.3% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-982 (1-23)

Qy 251 GlyHisProPheArgAlaTyr 257
Db 1 GGCCACCAUUCAGGCCAUU 21

RESULT 26
US-10-858-013-990
; Sequence 990, Application US/10858013
; Publication No. US2006013545A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09056
; CURRENT APPLICATION NUMBER: US/10/858,013
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide

US-09-544-776-2 (1-373) x US-10-858-013-990 (1-18)

Qy 143 ProProProProProPro 148
Db 1 CCGCCGCCGCCGCCGCCG 18

RESULT 27
US-10-858-164-990
; Sequence 990, Application US/10858164
; Publication No. US20060198828A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-07104
; CURRENT APPLICATION NUMBER: US/10/858,164
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
; US-10-858-013-990

Alignment Scores:
Pred. No.: 1.11e+05 Length: 18
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-858-013-990 (1-18)

Qy 143 ProProProProProPro 148
Db 1 CCGCCGCCGCCGCCGCCG 18

RESULT 27
US-10-858-164-990
; Sequence 990, Application US/10858164
; Publication No. US20060198828A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-07104
; CURRENT APPLICATION NUMBER: US/10/858,164
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
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US-10-858-164-990

Alignment Scores:
Pred. No.: 1.11e+05 Length: 18
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-858-164-990 (1-18)

QY 143 ProProProProProPro 148

Db 1 CCGCGCGCGCGCGCG 18

RESULT 28

US-10-858-146-990
; Sequence 990, Application US/10858146
; Publication No. US20060229267A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09057
; CURRENT APPLICATION NUMBER: US/10/858,146
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-146-990

Alignment Scores:
Pred. No.: 1.11e+05 Length: 18
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-858-146-990 (1-18)

QY 143 ProProProProProPro 148

Db 1 CCGCGCGCGCGCGCG 18

RESULT 29

US-11-301-360-559/c
; Sequence 559, Application US/11301360
; Publication No. US20060154890A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1037.70013US02
; CURRENT APPLICATION NUMBER: US/11/301,360
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 559
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-301-360-559

Alignment Scores:

Pred. No.: 1.17e+05 Length: 19
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-559 (1-19)

QY 143 ProProProProProPro 148

Db 18 CCGCGCGCGCGCGCCCC 1

RESULT 30

US-10-858-013-989
; Sequence 989, Application US/10858013
; Publication No. US20060135455A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, David
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09056
; CURRENT APPLICATION NUMBER: US/10/858,013
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)

```
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-013-989

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-858-013-989 (1-20)

QY 143 ProProProProPro 148
DB 1 CCGCGCGCGCGCGCGCG 18

RESULT 31
US-10-858-164-989
; Sequence 989, Application US/10858164
; Publication No. US20060198828A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-07104
; CURRENT APPLICATION NUMBER: US/10/858,164
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 989
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)..(14)
```

```
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-164-989

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-858-164-989 (1-20)

QY 143 ProProProProPro 148
DB 1 CCGCGCGCGCGCGCGCG 18

RESULT 32
US-10-668-050-133/c
; Sequence 133, Application US/10668050
; Publication No. US20060211639A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS AND
; TITLE OF INVENTION: CANCER MEDICAMENT COMBINATION THERAPY FOR THE TREATMENT OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: C1037.70052US00
; CURRENT APPLICATION NUMBER: US/10/668,050
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US 09/800,266
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,214
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-668-050-133

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x US-10-668-050-133 (1-20)

QY 143 ProProProProPro 148
DB 20 CCGCGCGCGCGCGCGCG 3

RESULT 33
US-10-858-146-989
; Sequence 989, Application US/10858146
; Publication No. US20060229267A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnejad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09057
```



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RESULT 34
US-11-248-241-3/c
; Sequence 3, Application US/11248241
; Publication No. US20060105366A1
; GENERAL INFORMATION:
; APPLICANT: Shinichi HIROSHIMA
; APPLICANT: Hiroshi TAKIGUCHI
; APPLICANT: Hitoshi FUKUSHIMA
; APPLICANT: Shinobu YOKOKAWA
; TITLE OF INVENTION: Specific Base Sequence Detection Method and Primer
; FILE REFERENCE: 125119
; CURRENT APPLICATION NUMBER: US/11/248,241
; CURRENT FILING DATE: 2005-10-13
; PRIOR APPLICATION NUMBER: JP 2004-331367
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:

```

```

Alignment Scores:
Pred. No.: 1.22e+05 20
Score: 42.00 6
Percent Similarity: 100.0% 0
Best Local Similarity: 100.0% 0
Query Match: 2.2% 0
DB: 8 0

US-09-544-776-2 (1-373) x US-11-254-920-12 (1-20)

Qy 143 ProProProProPro 148
|||||
Db 20 CCCCCCCCCCCCCCCC 3

RESULT 36
US-11-254-920-13
; Sequence 13, Application US/11254920
; Publication No. US20060135458A1
; GENERAL INFORMATION:
; APPLICANT: VAILLANT, Andrew
; APPLICANT: JUTEAU, Jean-Marie
; TITLE OF INVENTION: ANTIVIRAL OLIGONUCLEOTIDES
; FILE REFERENCE: 0999366-0000

```

; CURRENT APPLICATION NUMBER: US/11/254,920
 ; CURRENT FILING DATE: 2005-10-20
 ; PRIOR APPLICATION NUMBER: US 10/969,812
 ; PRIOR FILING DATE: 2004-10-19
 ; PRIOR APPLICATION NUMBER: US 60/668,983
 ; PRIOR FILING DATE: 2005-04-07
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: C20 oligomer
 ; FEATURE:
 ; NAME/KEY: misc_structure
 ; LOCATION: (1)...(20)
 ; OTHER INFORMATION: Phosphorothioate linkages
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (20)...(0)
 ; OTHER INFORMATION: FITC label
 US-11-254-920-13

Alignment Scores:
 Pred. No.: 1.22e+05 Length: 20
 Score: 42.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.2% Indels: 0
 DB: 8 Gaps: 0

US-09-544-776-2 (1-373) x US-11-254-920-13 (1-20)

Qy 143 ProProProProPro 148
 Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 37

; Sequence 243, Application US/11301360
 ; Publication No. US20060154890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Petersen, Deanna M.
 ; APPLICANT: Fouron, Yves
 ; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
 ; FILE REFERENCE: C1037.70013US02
 ; CURRENT APPLICATION NUMBER: US/11/301,360
 ; CURRENT FILING DATE: 2005-12-09
 ; PRIOR APPLICATION NUMBER: US 09/776,479
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: US 60/179,991
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 1093
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 243
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic sequence
 US-11-301-360-243

Alignment Scores:
 Pred. No.: 1.22e+05 Length: 20
 Score: 42.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.2% Indels: 0
 DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-243 (1-20)
 Qy 143 ProProProProPro 148
 Db 20 CCGCGCGCGCGCGCGC 3

RESULT 38

; Sequence 257, Application US/11301360
 ; Publication No. US20060154890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Petersen, Deanna M.
 ; APPLICANT: Fouron, Yves
 ; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
 ; FILE REFERENCE: C1037.70013US02
 ; CURRENT APPLICATION NUMBER: US/11/301,360
 ; CURRENT FILING DATE: 2005-12-09
 ; PRIOR APPLICATION NUMBER: US 09/776,479
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: US 60/179,991
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 1093
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 257
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic sequence
 US-11-301-360-257

Alignment Scores:
 Pred. No.: 1.22e+05 Length: 20
 Score: 42.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.2% Indels: 0
 DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-257 (1-20)

Qy 143 ProProProProPro 148
 Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 39

; Sequence 530, Application US/11301360
 ; Publication No. US20060154890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Petersen, Deanna M.
 ; APPLICANT: Fouron, Yves
 ; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
 ; FILE REFERENCE: C1037.70013US02
 ; CURRENT APPLICATION NUMBER: US/11/301,360
 ; CURRENT FILING DATE: 2005-12-09
 ; PRIOR APPLICATION NUMBER: US 09/776,479
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: US 60/179,991
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 1093
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 530
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic sequence
 US-11-301-360-530

```
Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-530 (1-20)

QY 143 ProProProProPro 148
DB 1 CCCCCCCCCCCCCCCCCC 18

RESULT 40
US-11-301-360-531/c
; Sequence 531, Application US/11301360
; Publication No. US20060154890A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1037.70013US02
; CURRENT APPLICATION NUMBER: US/11/301,360
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-301-360-531

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-531 (1-20)

QY 143 ProProProProPro 148
DB 20 CCCCCCCCCCCCCCCCCC 3

RESULT 41
US-11-301-360-811
; Sequence 811, Application US/11301360
; Publication No. US20060154890A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1037.70013US02
; CURRENT APPLICATION NUMBER: US/11/301,360
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
```

```
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 811
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-301-360-811

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-811 (1-20)

QY 143 ProProProProPro 148
DB 1 CCCCCCCCCCCCCCCCCC 18

RESULT 42
US-11-301-360-987/c
; Sequence 987, Application US/11301360
; Publication No. US20060154890A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1037.70013US02
; CURRENT APPLICATION NUMBER: US/11/301,360
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 987
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-301-360-987

Alignment Scores:
Pred. No.: 1.22e+05 Length: 20
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 9 Gaps: 0

US-09-544-776-2 (1-373) x US-11-301-360-987 (1-20)

QY 143 ProProProProPro 148
DB 20 CCCCCCCCCCCCCCCCCC 3

RESULT 43
US-11-339-222-920
; Sequence 920, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
```

```
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 920
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
; NAME/KEY: modified_base
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19
; OTHER INFORMATION: /mod_base = "2'-hydroxy corresponding base"
US-11-339-222-920

Alignment Scores:
Pred. No.: 1.28e+05 Length: 21
Score: 42.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-923 (1-21)
Qy 248 SerAspGluGlyHisProPhe 254
|||
Db 1 UCAGAUGAAGGCCACCAUUC 21

RESULT 45
US-11-339-222-1491
; Sequence 1491, Application US/11/339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutchek, Juergen
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 1491
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = uridine
; NAME/KEY: modified_base
; LOCATION: 1, 2, 6, 12, 13, 15, 16, 17, 19
; OTHER INFORMATION: /mod_base = "2'-O-methyl corresponding base"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 21
; OTHER INFORMATION: /mod_base = "5'-thio thymidine"
; NAME/KEY: modified_base
; LOCATION: 3, 4, 5, 7, 8, 9, 10, 11, 14, 18
; OTHER INFORMATION: /mod_base = "2'-hydroxy corresponding base"
US-11-339-222-1491

Alignment Scores:
Pred. No.: 1.28e+05 Length: 21
Score: 42.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 7 Gaps: 0

US-09-544-776-2 (1-373) x US-11-339-222-1491 (1-21)
Qy 248 SerAspGluGlyHisProPhe 254
|||
Db 1 UCAGAUGAAGGCCACCAUUC 21
```

RESULT 46

US-10-858-013-988
; Sequence 988, Application US/10858013
; Publication No. US20060135455A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09056
; CURRENT APPLICATION NUMBER: US/10/858,013
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 988
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
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; FEATURE:
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; LOCATION: (14)..(14)
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; LOCATION: (17)..(17)
; OTHER INFORMATION: methylated C nucleotide
; US-10-858-013-988

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DB: 6 Gaps: 0
US-10-858-013-988

US-09-544-776-2 (1-373) x US-10-858-013-988 (1-22)
QY 143 ProProProProPro 148
Db 1 CCGCGCGCGCGCGCGCG 18

RESULT 47

US-10-858-164-988
; Sequence 988, Application US/10858164
; Publication No. US2006019828A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-07104
; CURRENT APPLICATION NUMBER: US/10/858,164

; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 988
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)..(11)
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; US-10-858-164-988

Alignment Scores:
Pred. No.: 1.33e+05 Length: 22
Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 6 Gaps: 0
US-09-544-776-2 (1-373) x US-10-858-164-988 (1-22)

QY 143 ProProProProPro 148

Db 1 CCGCGCGCGCGCGCGCG 18

RESULT 48

US-10-858-146-988
; Sequence 988, Application US/10858146
; Publication No. US20060229267A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09057
; CURRENT APPLICATION NUMBER: US/10/858,146
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
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; SEQ ID NO 988
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (2)..(2)

US-10-858-146-988
; Sequence 988, Application US/10858146
; Publication No. US20060229267A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09057
; CURRENT APPLICATION NUMBER: US/10/858,146
; CURRENT FILING DATE: 2004-06-01
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; OTHER INFORMATION: methylated C nucleotide
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; NAME/KEY: modified_base
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; NAME/KEY: modified_base
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US-10-858-146-988
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Score: 42.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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US-09-544-776-2 (1-373) x US-10-858-146-988 (1-22)

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RESULT 49

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; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 919
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base = adenosine
US-11-339-222-919
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Alignment Scores:
Pred. No.: 1.38e+05 Length: 23
Score: 42.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 7 Gaps: 0
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US-09-544-776-2 (1-373) x US-11-339-222-919 (1-23)

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Oy 248 SerAspGluGlyHisProPhe 254
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RESULT 50

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; Sequence 922, Application US/11339222
; Publication No. US20060217324A1
; GENERAL INFORMATION:
; APPLICANT: Soutschek, Juergen
; TITLE OF INVENTION: RNAI MODULATION OF THE NOGO-L OR NOGO-R GENE AND USES THEREOF
; FILE REFERENCE: 14174-101001
; CURRENT APPLICATION NUMBER: US/11/339,222
; CURRENT FILING DATE: 2006-01-24
; PRIOR APPLICATION NUMBER: US 60/646,353
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/701,470
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/726,838
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: US 60/748,316
; PRIOR FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1624
; SEQ ID NO 922
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: siRNAs specific for Nogo-L
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Alignment Scores:
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Score: 42.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.2% Indels: 0
DB: 7 Gaps: 0
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US-09-544-776-2 (1-373) x US-11-339-222-922 (1-23)

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Oy 248 SerAspGluGlyHisProPhe 254
Db 3 UCAGAUGAGGCCACCCAUC 23
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Search completed: October 21, 2006, 05:49:22
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 21, 2006, 04:24:52 ; Search time 6830 Seconds
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Title: US-09-544-776-2

Perfect score: 1910

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Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	53	2.8	28	52	US-10-605-923-143953 Sequence 143953,
	4	53	2.8	28	52	US-10-605-924-592585 Sequence 592585,

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9	53	2.8	30	28	US-09-669-1877A-1096	Sequence 1096, Ap	c	82	48	2.5	27	48	US-10-310-914B-187729	Sequence 187729,
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13	53	2.8	30	50	US-10-433-899-9	Sequence 9, Appli	c	86	47	2.5	21	48	US-10-310-914A-1119929	Sequence 1119929,
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57	50	2.6	27	52	US-10-605-924-394517	Sequence 394517,	c	130	47	2.5	23	52	US-10-605-923-89913	Sequence 89913, A
58	50	2.6	27	54	US-10-707-975B-235549	Sequence 235549,	c	131	47	2.5	23	52	US-10-605-923-209976	Sequence 209976,
59	50	2.6	28	50	US-10-455-453-27	Sequence 27, Appli	c	132	47	2.5	23	52	US-10-605-923-470868	Sequence 470868,
60	50	2.6	30	1	PCT-US00-00325-397	Sequence 397, App	c	133	47	2.5	23	52	US-10-605-923-979624	Sequence 979624,
61	50	2.6	30	21	US-09-232-884-397	Sequence 397, App	c	134	47	2.5	23	52	US-10-605-924-400367	Sequence 400367,
62	50	2.6	30	41	US-10-101-487-1	Sequence 1, Appli	c	135	47	2.5	23	52	US-10-605-924-427716	Sequence 427716,
63	50	2.6	30	41	US-10-101-487-2	Sequence 2, Appli	c	136	47	2.5	23	52	US-10-605-924-624948	Sequence 624948,
64	50	2.6	30	41	US-10-101-487-63	Sequence 63, Appli	c	137	47	2.5	23	52	US-10-605-924-717695	Sequence 717695,
65	50	2.6	30	41	US-10-101-487-65	Sequence 65, Appli	c	138	47	2.5	23	52	US-10-605-924-734524	Sequence 734524,
66	50	2.6	30	48	US-10-310-914A-1168838	Sequence 1168838,	c	139	47	2.5	23	54	US-10-707-975B-231243	Sequence 231243,
67	50	2.6	30	48	US-10-310-914B-1168838	Sequence 1168838,	c	140	47	2.5	23	54	US-10-707-975B-409583	Sequence 409583,
68	50	2.6	30	52	US-10-605-924-1168838	Sequence 1168838,	c	141	47	2.5	23	54	US-10-707-975B-499583	Sequence 499583,
69	50	2.6	30	62	US-10-939-988-1	Sequence 1, Appli	c	142	47	2.5	24	48	US-10-310-914A-138910	Sequence 138910,
70	50	2.6	30	62	US-10-939-988-2	Sequence 2, Appli	c	143	47	2.5	24	48	US-10-310-914A-247848	Sequence 247848,
71	50	2.6	30	62	US-10-939-988-63	Sequence 63, Appli	c	144	47	2.5	24	48	US-10-310-914A-406855	Sequence 406855,
72	50	2.6	30	62	US-10-939-988-65	Sequence 65, Appli	c	145	47	2.5	24	48	US-10-310-914A-427729	Sequence 427729,
73	49	2.6	28	33	US-09-865-644-22	Sequence 22, Appli	c	146	47	2.5	24	48	US-10-310-914A-1310951	Sequence 1310951,
74	48	2.5	24	48	US-10-310-914A-632084	Sequence 632084,	c	147	47	2.5	24	48	US-10-310-914A-1310952	Sequence 1310952,
75	48	2.5	24	48	US-10-310-914B-632084	Sequence 632084,	c	148	47	2.5	24	48	US-10-310-914A-1323390	Sequence 1323390,
76	48	2.5	24	52	US-10-605-923-563928	Sequence 563928,	c	149	47	2.5	24	48	US-10-310-914B-138910	Sequence 138910,
77	48	2.5	24	52	US-10-605-924-632084	Sequence 632084,	c	150	47	2.5	24	48	US-10-310-914B-247848	Sequence 247848,


```

; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1433953
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-1433953

Alignment Scores:
Pred. No.: 2.31e+04 Length: 28
Score: 53.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.8% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-1433953 (1-28)
Qy 140 ProAlaArgProProProPro 148
Db 27 CCCCCTCGCGCGCGCGCGCGCGCG 1
RESULT 4
US-10-605-924-592585
; Sequence 592585, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592585
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-592585

Alignment Scores:
Pred. No.: 2.31e+04 Length: 28
Score: 53.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.8% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-924-592585 (1-28)
Qy 140 ProAlaArgProProProPro 148
Db 2 CCCCCTCGCGCGCGCGCGCGCGCG 28
RESULT 5
PCT-US03-11593-4
; Sequence 4, Application PC/TUS0311593
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane
; APPLICANT: Koehn, Richard
; APPLICANT: Patel, Dinesh
; TITLE OF INVENTION: Antiviral Compositions and Methods
; FILE REFERENCE: 3302.2.3
; CURRENT APPLICATION NUMBER: PCT/US03/11593
; CURRENT FILING DATE: 2003-04-16

ALIGNMENTS

RESULT 1
US-10-310-914A-592585
; Sequence 592585, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 592585
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-592585

Alignment Scores:
Pred. No.: 2.31e+04 Length: 28
Score: 53.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.8% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-592585 (1-28)
Qy 140 ProAlaArgProProProPro 148
Db 2 CCCCUCUGCGCGCGCGCGCGCGCG 28
RESULT 2
US-10-310-914B-592585
; Sequence 592585, Application US/10310914B
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 592585
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-592585

Alignment Scores:
Pred. No.: 2.31e+04 Length: 28
Score: 53.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.8% Indels: 0
DB: Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914B-592585 (1-28)
Qy 140 ProAlaArgProProProPro 148
Db 2 CCCCUCUGCGCGCGCGCGCGCGCG 28
RESULT 3
US-10-605-923-1433953/c
; Sequence 1433953, Application US/10605923
```

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US03-11593-4

Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 1 Gaps: 0

US-09-544-776-2 (1-373) x PCT-US03-11593-4 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 6

US-08-301-013-17/c
; Sequence 17, Application US/08301013
; GENERAL INFORMATION:
; APPLICANT: Makoto SEKI et al.
; TITLE OF INVENTION: ANTIVIRAL AGENT
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,013
; FILING DATE: September 6, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/299,113
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: Yes

US-08-301-013-17
Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0
DB: 12 Gaps: 0

US-09-544-776-2 (1-373) x US-08-301-013-17 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 7

US-08-589-911-9
; Sequence 9, Application US/08589911
; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P.
; TITLE OF INVENTION: Methods for screening for transdominant
; FILE REFERENCE: RIGL-004
; CURRENT APPLICATION NUMBER: US/08/589,911
; CURRENT FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-08-589-911-9

Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x US-08-589-911-9 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 8

US-08-589-911A-9
; Sequence 9, Application US/08589911A
; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P.
; TITLE OF INVENTION: Methods for screening for transdominant
; FILE REFERENCE: RIGL-004
; CURRENT APPLICATION NUMBER: US/08/589,911A
; CURRENT FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-08-589-911A-9

Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x US-08-589-911A-9 (1-30)

```
Qy 139 ProProAlaArgProProProProProPro 148
Db 1 CCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 30

RESULT 9
US-09-669-187A-1096
; Sequence 1096, Application US/09669187A
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/669,187A
; CURRENT FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1096
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-669-187A-1096

Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 28 Gaps: 0

US-09-544-776-2 (1-373) x US-09-669-187A-1096 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 10
US-10-057-467-12
; Sequence 12, Application US/10057467
; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P.
; APPLICANT: Rothenberg, Michael S.
; TITLE OF INVENTION: Methods for Screening for Transdominant
; Effector Peptides and RNA Molecules
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/057,467
; FILING DATE: 22-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/589,109
; FILING DATE: 23-JAN-1996

US-09-544-776-2 (1-373) x US-09-669-187A-1096 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 11
US-10-144-360-4
; Sequence 4, Application US/10144360
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane
; APPLICANT: Koehn, Richard
; APPLICANT: Patel, Dinesh
; TITLE OF INVENTION: Antiviral Compositions and Methods
; FILE REFERENCE: 3302.2.3
; CURRENT APPLICATION NUMBER: US/10/144,360
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-144-360-4

Alignment Scores:
Pred. No.: 2.61e+04 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 41 Gaps: 0

US-09-544-776-2 (1-373) x US-10-144-360-4 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 12
US-10-314-578-1096
; Sequence 1096, Application US/10314578
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
```

; APPLICANT: Vollmer, Jorg
 ; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
 ; FILE REFERENCE: C1039/7035 (HCL/MAT)
 ; CURRENT APPLICATION NUMBER: US/10/314,578
 ; CURRENT FILING DATE: 2002-12-09
 ; PRIOR APPLICATION NUMBER: US 60/156,113
 ; PRIOR FILING DATE: 1999-09-25
 ; PRIOR APPLICATION NUMBER: US 60/156,135
 ; PRIOR FILING DATE: 1999-09-27
 ; PRIOR APPLICATION NUMBER: US 60/227,436
 ; PRIOR FILING DATE: 2000-08-23
 ; NUMBER OF SEQ ID NOS: 1145
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1096
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Sequence
 US-10-314-578-1096

Alignment Scores:
 Pred. No.: 2.61e+04 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-314-578-1096 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 13

; Sequence 9, Application US/10433899
 ; GENERAL INFORMATION:
 ; APPLICANT: HAYASHIZAKI, Yoshihide
 ; TITLE OF INVENTION: METHOD FOR MALDI-TOF-MS ANALYSIS AND/OR SEQUENCING OF OLIGONUCLEOTIDES
 ; FILE REFERENCE: 0045-0303P
 ; CURRENT APPLICATION NUMBER: US/10/433,899
 ; CURRENT FILING DATE: 2003-12-08
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 30
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA 30mer
 ; NAME/KEY: modified base
 ; LOCATION: (30)..(30)
 ; OTHER INFORMATION: A T base is added onto the 3' end
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(30)
 ; OTHER INFORMATION: each CTP has an Fluoro substituent at the 2' position of the sugar
 US-10-433-899-9

Alignment Scores:
 Pred. No.: 2.61e+04 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 50 Gaps: 0

US-09-544-776-2 (1-373) x US-10-433-899-9 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 14

; Sequence 5, Application US/10479472A
 ; GENERAL INFORMATION:
 ; APPLICANT: DEL-FAVERO, JURGEN PETER LOE
 ; TITLE OF INVENTION: NOVEL BRAIN EXPRESSED GENE AND PROTEIN ASSOCIATED WITH
 ; TITLE OF INVENTION: BIPOLAR DISORDER
 ; FILE REFERENCE: JAB-1711
 ; CURRENT APPLICATION NUMBER: US/10/479,472A
 ; CURRENT FILING DATE: 2003-12-01
 ; PRIOR APPLICATION NUMBER: PCT/EP02/06316
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: EP 01202214.1
 ; PRIOR FILING DATE: 2001-06-11
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 5
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Illustrative
 ; OTHER INFORMATION: oligonucleotide
 US-10-479-472A-5

Alignment Scores:
 Pred. No.: 2.61e+04 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 50 Gaps: 0

US-09-544-776-2 (1-373) x US-10-479-472A-5 (1-30)

Qy 139 ProProAlaArgProProProProPro 148
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 15

; Sequence 6, Application US/10479472A
 ; GENERAL INFORMATION:
 ; APPLICANT: DEL-FAVERO, JURGEN PETER LOE
 ; TITLE OF INVENTION: NOVEL BRAIN EXPRESSED GENE AND PROTEIN ASSOCIATED WITH
 ; TITLE OF INVENTION: BIPOLAR DISORDER
 ; FILE REFERENCE: JAB-1711
 ; CURRENT APPLICATION NUMBER: US/10/479,472A
 ; CURRENT FILING DATE: 2003-12-01
 ; PRIOR APPLICATION NUMBER: PCT/EP02/06316
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: EP 01202214.1
 ; PRIOR FILING DATE: 2001-06-11
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 6
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Illustrative
 ; OTHER INFORMATION: oligonucleotide
 US-10-479-472A-6

Alignment Scores:
 Pred. No.: 2.61e+04 Length: 30
 Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservatives: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 50 Gaps: 0

US-09-544-776-2 (1-373) x US-10-479-472A-6 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 30 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1

RESULT 16

US-10-791-209A-6/c

; Sequence 6, Application US/10791209A

; GENERAL INFORMATION:

; APPLICANT: Hahn, Soonkap

; TITLE OF INVENTION: DETECTION OF STRP, SUCH AS FRAGILE X SYNDROME

; FILE REFERENCE: 81671

; CURRENT APPLICATION NUMBER: US/10/791,209A

; CURRENT FILING DATE: 2004-03-01

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; OTHER INFORMATION: Synthetic Probe

US-10-791-209A-6

Alignment Scores:

Pred. No.: 2.61e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservatives: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 60 Gaps: 0

US-09-544-776-2 (1-373) x US-10-791-209A-6 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 30 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1

RESULT 17

US-10-884-866-1096

; Sequence 1096, Application US/10884866

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Schetter, Christian

; TITLE OF INVENTION: Immunostimulatory Nucleic Acids

; FILE REFERENCE: C1039/7035 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/10/884,866

; CURRENT FILING DATE: 2004-07-02

; PRIOR APPLICATION NUMBER: US/09/669,187

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US 60/156,113

; PRIOR FILING DATE: 1999-09-25

; PRIOR APPLICATION NUMBER: US 60/156,135

; PRIOR FILING DATE: 1999-09-27

; PRIOR APPLICATION NUMBER: US 60/227,436

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 1145

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1096

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-10-884-866-1096

Alignment Scores:

Pred. No.: 2.61e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservatives: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 61 Gaps: 0

US-09-544-776-2 (1-373) x US-10-884-866-1096 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 18

US-10-888-803-1096

; Sequence 1096, Application US/10888803

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Schetter, Christian

; APPLICANT: Vollmer, Jorg

; TITLE OF INVENTION: Immunostimulatory Nucleic Acids

; FILE REFERENCE: C1039/7035 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/10/888,803

; CURRENT FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: US/09/669,187

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US 60/156,113

; PRIOR FILING DATE: 1999-09-25

; PRIOR APPLICATION NUMBER: US 60/156,135

; PRIOR FILING DATE: 1999-09-27

; PRIOR APPLICATION NUMBER: US 60/227,436

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 1145

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1096

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-10-888-803-1096

Alignment Scores:

Pred. No.: 2.61e+04 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservatives: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 61 Gaps: 0

US-09-544-776-2 (1-373) x US-10-888-803-1096 (1-30)

QY 139 ProProAlaArgProProProProPro 148

DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 19

US-10-310-914A-171952/c

; Sequence 171952, Application US/10310914A

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CFUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 171952

; LENGTH: 24


```
QY 139 ProProAlaArgProProPro 146
DB 1 CCUCCGCGCAGGCCCGCCGCCCT 24

RESULT 24
US-10-310-914B-1286261
; Sequence 1286261, Application US/10310914B
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvnzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286261
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1286261

Alignment Scores:
Pred. No.: 2.83e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914B-1286261 (1-24)

QY 141 AlaArgProProProProPro 148
DB 1 GCUCGGCCUCCUCCUCCUCCA 24

RESULT 25
US-10-605-923-526250/c
; Sequence 526250, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 526250
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-526250

Alignment Scores:
Pred. No.: 2.83e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-526250 (1-24)

QY 139 ProProAlaArgProProPro 146
DB 24 CCCCCGCGCCGCCCGCCGCCCT 1

RESULT 26
US-10-605-923-663007
; Sequence 663007, Application US/10605923
; GENERAL INFORMATION:
```

```
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 663007
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-663007

Alignment Scores:
Pred. No.: 2.83e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-663007 (1-24)

QY 139 ProProAlaArgProProPro 146
DB 1 CCACCTGCGCGCCACCGCCCT 24

RESULT 27
US-10-605-924-171952/c
; Sequence 171952, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171952
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-171952

Alignment Scores:
Pred. No.: 2.83e+04 Length: 24
Score: 51.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.7% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-924-171952 (1-24)

QY 139 ProProAlaArgProProPro 146
DB 24 CCACCTGCGCGCCACCGCCCT 1

RESULT 28
US-10-605-924-462664
; Sequence 462664, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 462664
```

```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-462664

Alignment Scores:
Pred. No.:      2.83e+04      Length:      24
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              52          Gaps:       0

US-09-544-776-2 (1-373) x US-10-605-924-462664 (1-24)

Qy      139 ProProAlaArgProProPro 146
      |||||
Db      1 CCTCCGCGCAGCGCCCGCCGCC 24

RESULT 29
US-10-605-924-1286261
; Sequence 1286261, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1286261
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-1286261

Alignment Scores:
Pred. No.:      2.83e+04      Length:      24
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              52          Gaps:       0

US-09-544-776-2 (1-373) x US-10-605-924-1286261 (1-24)

Qy      141 AlaArgProProProProPro 148
      |||||
Db      1 GCTCGGCTCTCTCTCTCTCTCCA 24

RESULT 30
US-10-707-975B-280099
; Sequence 280099, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Daniel, Kfar
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 280099
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-280099

Alignment Scores:
Pred. No.:      2.83e+04      Length:      24
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              54          Gaps:       0
```

```
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              54          Gaps:       0

US-09-544-776-2 (1-373) x US-10-707-975B-280099 (1-24)

Qy      139 ProProAlaArgProProPro 146
      |||||
Db      1 CCACCGCGCGCCACCGCCGCC 24

RESULT 31
US-10-707-975B-415874/c
; Sequence 415874, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Daniel, Kfar
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 415874
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-415874

Alignment Scores:
Pred. No.:      2.83e+04      Length:      24
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              54          Gaps:       0

US-09-544-776-2 (1-373) x US-10-707-975B-415874 (1-24)

Qy      139 ProProAlaArgProProPro 146
      |||||
Db      24 CCCCCGCGCGCCCGCCGCCCT 1

RESULT 32
US-10-707-975B-594674/c
; Sequence 594674, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Daniel, Kfar
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594674
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-594674

Alignment Scores:
Pred. No.:      2.83e+04      Length:      24
Score:          51.00         Matches:      8
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:     2.7%        Indels:      0
DB:              54          Gaps:       0
```


US-09-544-776-2 (1-373) x US-10-707-975B-594674 (1-24)

Qy 139 ProAlaArgProProPro 146

Db 24 CCACCTGCGGCCACCGCCCT 1

RESULT 33

US-10-310-914A-103505

; Sequence 103505, Application US/10310914A

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 103505

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-103505

Alignment Scores:

Pred. No.:	3.04e+04	Length:	25
Score:	51.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	48	Gaps:	0

US-09-544-776-2 (1-373) x US-10-310-914A-103505 (1-25)

Qy 140 ProAlaArgProProPro 147

Db 2 CCUGACGGCCUCCACCGCCCC 25

RESULT 34

US-10-310-914B-103505

; Sequence 103505, Application US/10310914B

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914B

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388411

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 103505

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914B-103505

Alignment Scores:

Pred. No.:	3.04e+04	Length:	25
Score:	51.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	48	Gaps:	0

US-09-544-776-2 (1-373) x US-10-310-914B-103505 (1-25)

Qy 140 ProAlaArgProProPro 147

Db 2 CCUGACGGCCUCCACCGCCCC 25

RESULT 35

US-10-605-924-103505

; Sequence 103505, Application US/10605924

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND

; FILE OF INVENTION: USES THEREOF

; FILE REFERENCE: 55004

; CURRENT APPLICATION NUMBER: US/10/605,924

; CURRENT FILING DATE: 2003-11-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 103505

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-605-924-103505

Alignment Scores:

Pred. No.:	3.04e+04	Length:	25
Score:	51.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	52	Gaps:	0

US-09-544-776-2 (1-373) x US-10-605-924-103505 (1-25)

Qy 140 ProAlaArgProProPro 147

Db 2 CCTGCACGGCTCCACCGCCCC 25

RESULT 36

US-10-707-975B-313723

; Sequence 313723, Application US/10707975B

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; APPLICANT: Bentwich, Itzhak

; APPLICANT: Daniel, Kfar

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND

; FILE OF INVENTION: USES THEREOF

; FILE REFERENCE: 06087.0201.CPUS01

; CURRENT APPLICATION NUMBER: US/10/707,975B

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 664008

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 313723

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-707-975B-313723

Alignment Scores:

Pred. No.:	3.04e+04	Length:	25
Score:	51.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.7%	Indels:	0
DB:	54	Gaps:	0

US-09-544-776-2 (1-373) x US-10-707-975B-313723 (1-25)

Qy 140 ProAlaArgProProPro 147

Db 2 CCUGACGGCCUCCACCGCCCC 25

RESULT 37

US-10-310-914A-1245216

; Sequence 1245216, Application US/10310914A

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1245216
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1245216

Alignment Scores:
Pred. No.: 3.48e+04 Length: 27
Score: 51.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.7% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1245216 (1-27)

Qy 139 ProProAlaAArgProProProPro 147
Db 1 CCGCCCGCGCGCGCGCGCGCGCGCG 27

RESULT 38

US-10-310-914B-1245216
; Sequence 1245216, Application US/10310914B
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1245216
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1245216

Alignment Scores:
Pred. No.: 3.48e+04 Length: 27
Score: 51.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.7% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914B-1245216 (1-27)

Qy 139 ProProAlaAArgProProProPro 147
Db 1 CCGCCCGCGCGCGCGCGCGCGCGCG 27

RESULT 39

US-10-605-923-1386500/c
; Sequence 1386500, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605.923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1386500
; LENGTH: 27

; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-1386500
Alignment Scores:
Pred. No.: 3.48e+04 Length: 27
Score: 51.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.7% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-1386500 (1-27)

Qy 139 ProProAlaAArgProProProPro 147
Db 27 CCGCCCGCGCGCGCGCGCGCGCGCG 1

RESULT 40

US-10-605-924-1245216
; Sequence 1245216, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605.924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1245216
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-1245216

Alignment Scores:
Pred. No.: 3.48e+04 Length: 27
Score: 51.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 2.7% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-924-1245216 (1-27)

Qy 139 ProProAlaAArgProProProPro 147
Db 1 CCGCCCGCGCGCGCGCGCGCGCGCG 27

RESULT 41

US-10-310-914A-394516/c
; Sequence 394516, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394516
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-394516

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-394516 (1-24)

QY 143 ProProProProProAlaSer 150

DB 24 CCGCGCGCGCGCGCGCGCATCT 1

RESULT 42

US-10-310-914A-1168845/c
; Sequence 1168845, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1168845
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1168845

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914A-1168845 (1-24)

QY 143 ProProProProProAlaSer 150

DB 24 CCGCGCGCGCGCGCGCGCTTCC 1

RESULT 43

US-10-310-914B-394516/c
; Sequence 394516, Application US/10310914B
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394516
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-394516

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914B-394516 (1-24)

QY 143 ProProProProProAlaSer 150

DB 24 CCGCGCGCGCGCGCGCGCATCT 1

RESULT 44

US-10-310-914B-1168845/c
; Sequence 1168845, Application US/10310914B
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1168845
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1168845

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 48 Gaps: 0

US-09-544-776-2 (1-373) x US-10-310-914B-1168845 (1-24)

QY 143 ProProProProProAlaSer 150

DB 24 CCGCGCGCGCGCGCGCGCTTCC 1

RESULT 45

US-10-605-923-201270
; Sequence 201270, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 201270
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-201270

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-201270 (1-24)

QY 143 ProProProProProAlaSer 150

DB 1 CCGCGCGCGCGCGCGCGCATCT 24

RESULT 46

US-10-605-923-1339216
; Sequence 1339216, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

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; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1339216
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-1339216

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-923-1339216 (1-24)

Qy 143 ProProProProProAlaSer 150
Db 1 CCGCGCGCGCGCGCGCGGCTTC 24

RESULT 47
US-10-605-924-394516/c
; Sequence 394516, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 394516
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-394516

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-924-394516 (1-24)

Qy 143 ProProProProProAlaSer 150
Db 24 CCGCGCGCGCGCGCGCGGCTTC 1

RESULT 48
US-10-605-924-1168845/c
; Sequence 1168845, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1168845
; LENGTH: 24
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-1168845

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 52 Gaps: 0

US-09-544-776-2 (1-373) x US-10-605-924-1168845 (1-24)

Qy 143 ProProProProProAlaSer 150
Db 24 CCGCGCGCGCGCGCGGCTTC 1

RESULT 49
US-10-707-975B-185055/c
; Sequence 185055, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185055
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-185055

Alignment Scores:
Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.8% Indels: 0
DB: 54 Gaps: 0

US-09-544-776-2 (1-373) x US-10-707-975B-185055 (1-24)

Qy 143 ProProProProProAlaSer 150
Db 24 CCGCGCGCGCGCGCGGCTTC 1

RESULT 50
US-10-707-975B-243848
; Sequence 243848, Application US/10707975B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 06087.0201.CPUS01
; CURRENT APPLICATION NUMBER: US/10/707,975B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 664008
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 243848
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-707-975B-243848

Alignment Scores:
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Pred. No.: 3.59e+04 Length: 24
Score: 50.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.6% Indels: 0
DB: 54 Gaps: 0

US-09-544-776-2 (1-373) x US-10-707-975B-243848 (1-24)

Qy 143 ProProProProProProHlaSer 150

Db 1 CCGCGCGCGCGCGCGCGCGCGCGCAUCU 24

Search completed: October 21, 2006, 07:55:36
Job time : 6834 secs

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GenCore version 5.1.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 21, 2006, 04:08:21 ; Search time 779 Seconds

(without alignments)
5007.668 Million cell updates/sec

Title: US-09-544-776-2

Perfect score: 1910

Sequence: 1 MEDLQSLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 373

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4440446

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-LIST=150 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	2.8	30	6	Abk10417 Synthetic
3	53	2.8	30	6	Abk10411 Synthetic

Abx04111 Oligonucl	30	10	ABX04111	2.8	53
Adf82757 Antiviral	30	12	ADF82757	2.8	53
Adu87448 Target ge	30	13	ADU87448	2.8	53
Aeb28261 Oligonucl	30	14	AEb28261	2.8	53
Aec37003 Phosphodi	30	14	AEC37003	2.8	53
Aec14081 Human PRA	30	14	AEC14081	2.8	53
Aee47860 Human Y c	30	15	AEE47860	2.8	53
Abk95215 PCR prime	28	6	ABK95215	2.6	50
Abn81202 Litopenae	30	3	ABN81202	2.6	50
Abz22047 Polyani	30	10	ABZ22047	2.6	50
Abz22048 Polyani	30	10	ABZ22048	2.6	50
Abz22086 Polyani	30	10	ABZ22086	2.6	50
Aai43651 Human tel	28	6	AAL43651	2.6	49
Adp17616 Renal cel	25	12	ADP17616	2.5	47
Aat09304 Murine an	30	2	AAT09304	2.5	47
Aaa74323 Loblolly	30	3	AAA74323	2.5	47
Aed96668 Human C-r	24	14	AED96668	2.4	46
Aaq40855 DNA seque	27	2	AAQ40855	2.4	46
Aaq40856 DNA seque	27	2	AAQ40856	2.4	46
Adv96473 CGG repea	27	14	ADV96473	2.4	46
Aaq41910 erb B2/ne	28	2	AAQ41910	2.4	46
Aaq88043 CU-rich t	28	2	AAQ88043	2.4	46
Aav08947 PCR prime	28	2	AAV08947	2.4	46
Aav02972 Hepatitis	28	2	AAV02972	2.4	46
Aav44665 Triplex-f	28	2	AAV44665	2.4	46
Aaf99570 Immunosti	28	4	AAF99570	2.4	46
Abf78286 Angiogene	28	6	ABF78286	2.4	46
Ab138794 Immunosti	28	6	ABL38794	2.4	46
Ach03108 Immunosti	28	9	ACH03108	2.4	46
Adb37072 Immunosti	28	9	ADB37072	2.4	46
Adf82756 Antiviral	28	12	ADF82756	2.4	46
Adu90086 Allergic	28	13	ADU90086	2.4	46
Aed75539 Immunosti	28	14	AED75539	2.4	46
Aac63576 Guanosine	29	3	AAC63576	2.4	46
Adf64858 Non-antis	29	10	ADF64858	2.4	46
Adi28707 Guanosine	29	12	ADI28707	2.4	46
Ady53899 Non-antis	29	14	ADY53899	2.4	46
Adz58621 Inflammat	29	14	ADZ58621	2.4	46
Aaq20873 Immunosti	30	2	AAQ20873	2.4	46
Aaq20870 Immunosti	30	2	AAQ20870	2.4	46
Aaq81071 supf gene	30	2	AAQ81071	2.4	46
Aat70013 Triplex-f	30	2	AAT70013	2.4	46
Aat47060 Oligonucl	30	2	AAT47060	2.4	46
Aax27663 DNA encod	30	2	AAX27663	2.4	46
Abn81202 Litopenae	30	3	ABN81202	2.4	46
Aaa05780 Streptavi	30	3	AAA05780	2.4	46
Aai65861 Nucleotid	30	4	AAI65861	2.4	46
Aah20276 Gol9 link	30	4	AAH20276	2.4	46
Abk99277 Hepatitis	30	6	ABK99277	2.4	46
Abf74266 Transloca	30	6	ABF74266	2.4	46
Ab151730 HRGP rela	30	6	ABL51730	2.4	46
Ab151739 Hydroxypr	30	6	ABL51739	2.4	46
Abx80007 EST polym	30	8	ABX80007	2.4	46
Acf05808 Synthetic	30	9	ACF05808	2.4	46
Adh44688 DNA tripl	30	12	ADH44688	2.4	46
Adu09143 Ser-HYP4	30	13	ADU09143	2.4	46
Adu09116 Hydroxypr	30	13	ADU09116	2.4	46
Adv97059 Chimeric	30	14	ADV97059	2.4	46
Aat99285 POLYG, a	24	2	AAT99285	2.4	45
Aav31742 Nucleotid	24	2	AAV31742	2.4	45
Aax04085 Oligonucl	24	2	AAx04085	2.4	45
Aac64410 Human Nog	24	3	AAc64410	2.4	45
Aah46049 Synthetic	24	4	AHA46049	2.4	45
Aaf99299 Immunosti	24	4	AAF99299	2.4	45
Aaf99758 Immunosti	24	4	AAF99758	2.4	45
Abf78479 Angiogene	24	6	ABF78479	2.4	45
Abf77944 Angiogene	24	6	ABF77944	2.4	45
Ab138793 Immunosti	24	6	ABL38793	2.4	45
Abk03286 Immunosti	24	9	ABK03286	2.4	45
Adc99724 Immunosti	24	9	ADC99724	2.4	45
Adb36801 Immunosti	24	9	ADB36801	2.4	45
Adb37260 Immunosti	24	9	ADB37260	2.4	45

77	45	2.4	24	12	ADP82754	Adf82754 Antiviral	150	42	2.2	18	2	AAQ79242	Aaq79242 Guanosine
78	45	2.4	24	12	ADN97166	Adn97166 Probe of							
79	45	2.4	24	13	ADR48247	Adr48247 Microarra							
80	45	2.4	24	13	ADR48248	Adr48248 Microarra							
81	45	2.4	24	13	ADU89744	Adu89744 Allergic							
82	45	2.4	24	13	ADU90279	Adu90279 Allergic							
83	45	2.4	24	14	ADP75712	Adp75712 Immunosti							
84	45	2.4	24	14	ADP75274	Adp75274 Immunosti							
85	45	2.4	25	2	AAQ55856	Aaq55856 Fragile X							
86	45	2.4	25	2	AAQ85271	Aaq85271 Probe for							
87	45	2.4	25	2	AAQ76435	Aax76435 Sequencin							
88	45	2.4	25	2	AAQ05267	Aax05267 Fragile X							
89	45	2.4	26	1	AAH81251	Aan81251 Probe O-C							
90	45	2.4	26	1	AAH82048	Aan82048 Probe O-C							
91	45	2.4	26	1	AAH82052	Aaq47177 MHC DR A							
92	45	2.4	26	1	AAQ47176	Aaq47177 MHC DR A							
93	45	2.4	26	2	AAQ91051	Aag30051 IFN-gamma							
94	45	2.4	26	2	AAQ91051	Adf82755 Antiviral							
95	45	2.4	26	12	ADP82755	Aec36496 TGF-beta1							
96	45	2.4	26	14	AEC36496	Aec36501 TGF-beta1							
97	45	2.4	26	14	AEC36501	Aah46019 Synthetic							
98	45	2.4	27	4	AAH46019	Aah46003 Synthetic							
99	45	2.4	27	4	AAH46003	Adt99607 Quadruple							
100	45	2.4	27	13	ADT99607	Adt92600 Quadruple							
101	45	2.4	27	13	ADT92600	Aec36534 TGF-beta1							
102	45	2.4	27	14	AEC36534	Aec36497 TGF-beta1							
103	45	2.4	28	2	AAQ25474	Aaq25474 Purine ri							
104	45	2.4	28	2	AAQ70677	Aaq70677 Purine ri							
105	45	2.4	28	2	AAV44666	Av44666 Her-2/neu							
106	45	2.4	28	2	AAV44666	Ad58099 Barley BA							
107	45	2.4	28	9	AD58099	Ad58099 Barley BA							
108	45	2.4	28	9	AD58099	Ado30693 Quadruple							
109	45	2.4	28	12	AD30693	Adz67890 Quadruple							
110	45	2.4	28	14	ADZ67890	Adt47059 Triplex t							
111	45	2.4	30	2	AAQ76421	Aax76421 Sequencin							
112	45	2.4	30	2	AAQ76421	Aao5777 Streptavi							
113	45	2.4	30	3	AAQ05777	Acf05809 Synthetic							
114	45	2.4	30	9	ACF05809	Abx04111 Oligonucl							
115	45	2.4	30	10	ABX04111	Adh44690 Triple he							
116	45	2.4	30	12	ADH44690	Adp17618 Renal cel							
117	44	2.3	25	12	ADP17618	Adt76330 Human mus							
118	44	2.3	25	2	AAQ76330	Aax54129 Muscarini							
119	44	2.3	27	2	AAQ54129	Aaa33573 Low adeno							
120	44	2.3	27	3	AAA33573	Aaf19695 Human mus							
121	44	2.3	27	3	AAF19695	Abz95389 Human mus							
122	44	2.3	27	10	ABZ95389	Abd19435 Human mus							
123	44	2.3	27	11	ABD19435	Aat51631 Viral int							
124	44	2.3	30	2	AAQ51631	Aag96455 Human cyc							
125	44	2.3	30	4	AAQ96455	Adf55332 PCR prime							
126	44	2.3	30	4	AAF55332	Adx15550 Cyclin E							
127	44	2.3	30	14	ADX15550	Adp29145 Human sec							
128	43	2.3	21	12	ADP29145	Abz04964 Human FD1							
129	43	2.3	24	6	ABA04964	Aal49457 Mutation							
130	43	2.3	27	6	AAQ49457	Aac63375 Guanosine							
131	43	2.3	29	3	AAQ63375	Aac63377 Guanosine							
132	43	2.3	29	3	AAQ63377	Aad64859 Non-antis							
133	43	2.3	29	10	AD64859	Aad64857 Non-antis							
134	43	2.3	29	10	AD64857	Adi28706 Guanosine							
135	43	2.3	29	12	ADI28706	Ady53900 Non-antis							
136	43	2.3	29	12	ADY53900	Adz58620 Inflammat							
137	43	2.3	29	14	ADY53898	Adz58622 Inflammat							
138	43	2.3	29	14	ADZ58620	Aac31897 PCR prime							
139	43	2.3	29	14	ADZ58622	Aaz56862 Fish IGF-							
140	43	2.3	30	2	AAQ31897	Aaa55218 G+C rich							
141	43	2.3	30	2	AAQ31897	Aaf86670 Tilapia I							
142	43	2.3	30	3	AAQ56862	Adc66453 Human Fra							
143	43	2.3	30	3	AAQ55218	Adc66453 Human Fra							
144	43	2.3	30	4	AAF86670	Adc66453 Human Fra							
145	43	2.3	30	10	AD66453	Adc66453 Human Fra							
146	43	2.3	30	10	AD66453	Adc66453 Human Fra							
147	43	2.3	30	14	AD66453	Adz67883 Quadruple							
148	43	2.3	30	14	AD66453	Aaa39364 Cyclin D1							
149	42	2.2	18	2	AAQ70698	Aaq70698 C-Rich ol							

ALIGNMENTS

RESULT 1

AAQ99890 standard; DNA; 30 BP.

AAQ99890; 12-JUN-2001 (first entry)

Immunostimulatory nucleic acid #1006.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Synthetic.

WO200122972-A2.

05-APR-2001.

25-SEP-2000; 2000WO-US026383.

25-SEP-1999; 99US-0156113P.

27-SEP-1999; 99US-0156135P.

23-AUG-2000; 2000US-0227436P.

(IOWA) UNIV IOWA RES FOUND.

(COLE-) COLEY PHARM GMBH.

Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.

Example 6; Page 60; 339pp; English.

The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone

Sequence 30 BP; 0 A; 30 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.: 1.49e+05 Length: 30

Score: 53.00 Matches: 8

Percent Similarity: 80.0% Conservative: 0

Best Local Similarity: 80.0% Mismatches: 2

Query Match: 2.8% Indels: 0

DB: 4 Gaps: 0

US-09-544-776-2 (1-373) x AAF99890 (1-30)

QY 139 ProProXlaArgProProProProProPro 148

||||| ||||||||||||||||


```
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30
RESULT 2
ABK10417/c
ID ABK10417 standard; DNA; 30 BP.
XX AC ABK10417;
XX DT 21-MAY-2002 (first entry)
XX DE Synthetic primer sequence 5'-G30-3'.
XX KW ss; 5'-G30-3'; double stranded DNA generation; promiscuous base;
XX KW target molecule; primer.
XX OS Synthetic.
XX PN US6326143-B1.
XX PD 04-DEC-2001.
XX PF 22-MAY-1998; 98US-00083123.
XX PR 22-NOV-1996; 96WO-EP005149.
XX PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PI Orum H, Seeger C;
XX DR WPI; 2002-214947/27.
XX PT Determining an analyte in a sample, for generating multiple double
XX PT stranded nucleic acids, comprises employing a single primer sequence with
XX PT a nucleobase sequence having affinity to the sequence contained in a
XX PS target nucleic acid.
XX PS Example 1; Col 14; 25pp; English.
XX CC The invention relates to determining an analyte in a sample comprising
XX CC (a) providing a target nucleic acid comprising a region A, a nucleobase
XX CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
XX CC analyte, and the region A specifically binds to the analyte, (b) binding
XX CC the target nucleic acid to the analyte, separating the analyte bound to
XX CC the target nucleic acid from the remaining part of the sample, (d)
XX CC hybridising a primer to the target nucleic acid, where the primer
XX CC comprises a nucleobase sequence B', and the nucleobase sequence B'
XX CC hybridises to the nucleobase sequence B, (e) elongating the hybridised
XX CC primer to produce an elongation product E using the target nucleic acid
XX CC as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base which is capable of
XX CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
XX CC separating the target nucleic acid from the elongation product E, (g)
XX CC hybridising a further primer which comprises the nucleobase sequence B'
XX CC to the elongation product E, where the elongation product E is capable of
XX CC acting as a template for the elongation of the further primer, (h)
XX CC elongating the hybridised further primer of step (g) to produce an
XX CC elongation product E' using the elongation product E as a template and
XX CC using nucleotides, where at least 30 % of the nucleotides contain at
XX CC least one promiscuous base, (i) separating the elongation product E from
XX CC the elongation product E', (j) hybridising a further primer comprising a
XX CC nucleobase sequence B' to the target nucleic acid or the elongation
XX CC product E, (k) elongating the further primer of step (j) to produce
XX CC another elongation product E using the target nucleic acid or elongation
XX CC product E as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base, (l) separating product
XX CC E of step (k) from the target nucleic acid or elongation product E, (m)
XX CC optionally repeating steps (g) - (l) a sufficient number of times to
XX CC generate a desired amount of double stranded nucleic acids and (n)
XX CC determining the elongation product E and/or elongation product E' as a
XX CC measure of the presence or amount of the analyte, where the lengths of
XX CC the sequence I and the nucleobase sequence B are chosen such that, when
XX CC the further primer hybridises to the elongation product E in step (g),
CC the further primer spans a sequence formed by elongation of the
CC hybridised primer of step (e) and overlaps at least a part of the 3'
CC region of the hybridized primer of step (e) by an overlap length. The
CC method is useful for determining an analyte in a sample. In particular, the
CC method is useful for generating multiple double stranded nucleic acids.
CC The present sequence is a primer molecule used to exemplify the method of
CC the invention
XX SQ Sequence 30 BP; 0 A; 0 C; 30 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x ABK10417 (1-30)
QY 139 ProProAlaArgProProProProProPro 148
Db 30 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1
RESULT 3
ABK10411
ID ABK10411 standard; DNA; 30 BP.
XX AC ABK10411;
XX DT 21-MAY-2002 (first entry)
XX DE Synthetic primer sequence 5'-C30-3'.
XX KW ss; 5'-C30-3'; double stranded DNA generation; promiscuous base;
XX KW target molecule; primer.
XX OS Synthetic.
XX PN US6326143-B1.
XX PD 04-DEC-2001.
XX PF 22-MAY-1998; 98US-00083123.
XX PR 22-NOV-1996; 96WO-EP005149.
XX PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PI Orum H, Seeger C;
XX DR WPI; 2002-214947/27.
XX PT Determining an analyte in a sample, for generating multiple double
XX PT stranded nucleic acids, comprises employing a single primer sequence with
XX PT a nucleobase sequence having affinity to the sequence contained in a
XX PT target nucleic acid.
XX PS Example 1; Col 14; 25pp; English.
XX CC The invention relates to determining an analyte in a sample comprising
XX CC (a) providing a target nucleic acid comprising a region A, a nucleobase
XX CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
XX CC analyte, and the region A specifically binds to the analyte, (b) binding
XX CC the target nucleic acid to the analyte, separating the analyte bound to
XX CC the target nucleic acid from the remaining part of the sample, (d)
XX CC hybridising a primer to the target nucleic acid, where the primer
XX CC comprises a nucleobase sequence B', and the nucleobase sequence B'
XX CC hybridises to the nucleobase sequence B, (e) elongating the hybridised
XX CC primer to produce an elongation product E using the target nucleic acid
XX CC as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base which is capable of
XX CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
XX CC separating the target nucleic acid from the elongation product E, (g)
XX CC hybridising a further primer which comprises the nucleobase sequence B'
XX CC to the elongation product E, where the elongation product E is capable of
XX CC acting as a template for the elongation of the further primer, (h)
XX CC elongating the hybridised further primer of step (g) to produce an
XX CC elongation product E' using the elongation product E as a template and
XX CC using nucleotides, where at least 30 % of the nucleotides contain at
XX CC least one promiscuous base, (i) separating the elongation product E from
XX CC the elongation product E', (j) hybridising a further primer comprising a
XX CC nucleobase sequence B' to the target nucleic acid or the elongation
XX CC product E, (k) elongating the further primer of step (j) to produce
XX CC another elongation product E using the target nucleic acid or elongation
XX CC product E as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base, (l) separating product
XX CC E of step (k) from the target nucleic acid or elongation product E, (m)
XX CC optionally repeating steps (g) - (l) a sufficient number of times to
XX CC generate a desired amount of double stranded nucleic acids and (n)
XX CC determining the elongation product E and/or elongation product E' as a
XX CC measure of the presence or amount of the analyte, where the lengths of
XX CC the sequence I and the nucleobase sequence B are chosen such that, when
XX CC the further primer hybridises to the elongation product E in step (g),
```

CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
 CC separating the target nucleic acid from the elongation product E, (g)
 CC hybridising a further primer which comprises the nucleobase sequence B'
 CC to the elongation product E, where the elongation product E is capable of
 CC acting as a template for the elongation of the further primer, (h)
 CC elongating the hybridised further primer of step (g) to produce an
 CC elongation product E' using the elongation product E as a template and
 CC using nucleotides, where at least 30 % of the nucleotides contain at
 CC least one promiscuous base, (i) separating the elongation product E from
 CC the elongation product E', (j) hybridising a further primer comprising a
 CC nucleobase sequence B' to the target nucleic acid or the elongation
 CC product E, (k) elongating the further primer of step (j) to produce
 CC another elongation product E using the target nucleic acid or elongation
 CC product E as a template and using nucleotides, where at least 30 % of the
 CC nucleotides contain at least one promiscuous base, (l) separating product
 CC E of step (k) from the target nucleic acid or elongation product E, (m)
 CC optionally repeating steps (g) - (l) a sufficient number of times to
 CC generate a desired amount of double stranded nucleic acids and (n)
 CC determining the elongation product E and/or elongation product E' as a
 CC measure of the presence or amount of the analyte, where the lengths of
 CC the sequence I and the nucleobase sequence B are chosen such that, when
 CC the further primer hybridises to the elongation product E in step (g),
 CC the further primer spans a sequence formed by elongation of the
 CC hybridised primer of step (e) and overlaps at least a part of the 3'
 CC region of the hybridized primer of step (e) by an overlap length. The
 CC method is useful for determining an analyte in a sample. In particular, the
 CC method is useful for generating multiple double stranded nucleic acids.
 CC The present sequence is a primer molecule used to exemplify the method of
 CC the invention

SQ Sequence 30 BP; 0 A; 30 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.49e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x ABK10411 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 4

ABX04111

ID ABX04111 standard; DNA; 30 BP.

XX AC ABX04111;

XX DT 13-JAN-2003 (first entry)

XX DE Oligonucleotide for creation of peptides controlling signal pathways #18.

XX KW Transdominant intercellular bioactive agent; cancer; tumour; apoptosis;
 KW cell death; cell division; cell growth; brca-1; brca-2;
 KW tumour suppressor; adenomatous polyposis coli gene; cardiovascular;
 KW arrhythmia; heart failure; neurobiology; endocrinology; immunobiology;
 KW stroke; infectious disease; bone; inflammation; allergic response;
 KW atherosclerosis; obesity; skin biology application; ds.

XX OS Synthetic.

XX PN US2002127564-A1.

XX PD 12-SEP-2002.

XX PF 27-JUL-2001; 2001US-00916940.

XX PR 23-JAN-1996; 96US-00589109.

XX PR 23-JAN-1996; 96US-00589911.

PR 23-JAN-1997; 97US-00787738.
 PR 23-JAN-1997; 97US-00789333.
 PR 13-NOV-1997; 97US-00963368.
 PR 28-NOV-2000; 2000US-00727715.
 XX (NOLA/) NOLAN G P.

XX PI Nolan GP;

XX DR WPI; 2003-028932/02.

XX PT Screening for transdominant bioactive agents capable of altering
 PT phenotype of a cell, by introducing library of randomized candidate
 PT nucleic acids into several cells and selecting cells exhibiting altered
 PT phenotype.

PS Example 2; Fig 2; 38pp; English.

XX CC The invention describes a method of screening (M) for a transdominant
 CC intercellular bioactive agent capable of altering phenotype of a cell,
 CC comprising introducing a molecular library of randomised candidate
 CC nucleic acids into several cells, where each of the nucleic acids
 CC comprises a different nucleotide sequence and screening the cells for a
 CC cell exhibiting an altered phenotype, where the altered phenotype is due
 CC to presence of a transdominant bioactive agent. The bioactive agent or
 CC the nucleic acid encoding it are useful to identify target molecules,
 CC i.e. the molecules with which the bioactive agent interacts. (M) is
 CC useful in: cancer applications by introducing random libraries into any
 CC tumour cell and identifying peptides which induce apoptosis, cell
 CC death, loss of cell division or decreased cell growth; for screening of
 CC bioactive agents which restore the constitutive function of the brca-1 or
 CC brca-2 genes, and other tumour suppressor genes important in breast
 CC cancer such as the adenomatous polyposis coli gene; in cardiovascular
 CC applications; screening for diminished arrhythmia potential in
 CC cardiomyocytes; for enhanced contractile properties of cardiomyocytes and
 CC diminished heart failure potential and is useful in neurobiology,
 CC endocrinology, immunobiology, arrhythmias, treatment of stroke,
 CC infectious disease, bone, inflammation, allergic response,
 CC atherosclerosis, obesity and skin biology applications. (M) allows rapid screening
 CC of large numbers of random oligonucleotides and their corresponding the
 CC expression products in a single, in vivo step. Thus, by delivering the
 CC random oligonucleotides to cells and screening the same cells, without
 CC the need to collect or synthesize in vitro the candidate agents, highly
 CC efficient screening is accomplished. In addition, the method allows
 CC screening in the absence of significant prior characterisation of the
 CC cellular defect. This sequence represents an oligonucleotide used for
 CC creating peptides used in the control of signal pathways within cells

SQ Sequence 30 BP; 0 A; 20 C; 0 G; 10 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e+05 Length: 30
 Score: 53.00 Matches: 8
 Percent Similarity: 80.0% Conservative: 0
 Best Local Similarity: 80.0% Mismatches: 2
 Query Match: 2.8% Indels: 0
 DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x ABX04111 (1-30)

Qy 139 ProProAlaArgProProProProProPro 148

Db 1 CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 30

RESULT 5

ADF82757

ID ADF82757 standard; DNA; 30 BP.

XX AC ADF82757;

XX DT 26-FEB-2004 (first entry)

```
DE Antiviral phosphorothioate oligonucleotide.
XX
KW Anti-HIV; virucide; antiviral; phosphorothioate; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..30
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= phosphorothioate nucleotides"
XX
PN WO2003097661-A2.
XX
PD 27-NOV-2003.
XX
PP 16-APR-2003; 2003WO-US011593.
XX
PR 13-MAY-2002; 2002US-00144360.
XX
PA (SALU-) SALUS THERAPEUTICS.
XX
PI Chen Z, Ruffner D, Koehn R, Patel D;
XX
PS WPI; 2004-012521/01.
XX
XX New pharmaceutical composition comprising an oligonucleotide having a
PT phosphorothioate inter-sugar linkage, useful for inhibiting the
PT replication of a retrovirus, particularly HIV-1 or HIV-2.
XX
XX Example 4; SEQ ID NO 4; 38pp; English.
XX
CC The present sequence is that of a 30-mer homopolydeoxycytidine. This is
CC an example of antiviral phosphorothioate oligonucleotides of the
CC invention ADF82757-ADP82773 that are used in claimed pharmaceutical
CC compositions for inhibiting the replication of a retrovirus, particularly
CC HIV-1 or HIV-2. The antiviral phosphorothioate oligonucleotides optimally
CC have a chain length of 32-50, especially 36-40, nucleotides, and may
CC comprise a 3' inverted thymine base.
XX
SQ Sequence 30 BP; 0 A; 30 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 12 Gaps: 0

US-09-544-776-2 (1-373) x ADF82757 (1-30)

QY 139 ProProAlaArgProProProProPto 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 6
ADU87448
ID ADU87448 standard; DNA; 30 BP.
XX
AC ADU87448;
XX
DT 10-FEB-2005 (first entry)
XX
DE Target gene extraction method associated dC30-N probe.
XX
KW Target gene; DNA purification; hybridization; cloning; DNA library;
KW probe; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 30
```

```
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "Modified by NH2 group"
XX
PN WO2004101785-A1.
XX
PD 25-NOV-2004.
XX
PP 27-APR-2004; 2004WO-JP006108.
XX
PR 13-MAY-2003; 2003JP-00134960.
XX
XX (JAPS ) JSR CORP.
XX (ENOW/) ENOMOTO T.
XX Enomoto T, Fan K;
XX
DR WPI; 2004-834007/82.
XX
XX Extracting target gene, by mixing sample with particles having probe DNA
PT and single-stranded bridge oligonucleotide having sequences complementary
PT to probe and target gene, and hybridizing particle, oligonucleotide and
PT target gene.
XX
XX Example 1; Page 8; 28pp; Japanese.
XX
CC The invention relates to a method of extracting a target gene. The method
CC involves mixing particles having a probe DNA bound to its surface, a
CC single-stranded bridge oligonucleotide having at one side a sequence
CC complementary to the probe DNA and at the other side a sequence
CC complementary to a part of a base sequence of target gene and a sample
CC containing target gene to be extracted, and hybridizing the probe DNA,
CC the single-stranded bridge oligonucleotide and the target gene. The
CC method is useful for extracting, separating, purifying and detecting
CC target DNA from gene cloning and cDNA libraries. The method of extracting
CC target DNA using the particle having the bound probe DNA is extremely
CC simple and easy. The target DNA can be extracted accurately and
CC efficiently without being influenced by the configuration and size of the
CC target gene, and the screening process can be accomplished within 24
CC hours. This sequence represents a probe used in the examples of the
CC present invention.
XX
SQ Sequence 30 BP; 0 A; 30 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e+05 Length: 30
Score: 53.00 Matches: 8
Percent Similarity: 80.0% Conservative: 0
Best Local Similarity: 80.0% Mismatches: 2
Query Match: 2.8% Indels: 0
DB: 13 Gaps: 0

US-09-544-776-2 (1-373) x ADU87448 (1-30)

QY 139 ProProAlaArgProProProPro 148
Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 7
AEB28261
ID AEB28261 standard; DNA; 30 BP.
XX
AC AEB28261;
XX
DT 22-SEP-2005 (first entry)
XX
DE Oligonucleotide 100C-PTO (30mer).
XX
KW cosmetics; pharmaceutical; skin allergy; dermatological;
KW dermatological disease; antiinflammatory; antiallergic; aging; eczema;
KW alopecia; epidermolysis bullosa; graft rejection; periodontal disease;
KW psoriasis; antipsoriatic; sunburn; vitiligo; inflammation; detergent;
KW dye; pigment; ss; primer; phosphorothioate.
```

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 1..30

XX FT /*tag= a

XX FT /mod_base= OTHER

XX FT /note= "phosphorothioate linkages"

XX PN WO2005063300-A2.

XX PD 14-JUL-2005.

XX PF 14-DEC-2004; 2004WO-EP014195.

XX PR 23-DEC-2003; 2003DE-01061502.

XX PA (PHEN-) PHENION GMBH & CO KG.

XX PI Kippenberger S, Kaufmann R, Bernd A, Bock A;

XX DR WPI; 2005-512612/52.

XX PT Cosmetic or pharmaceutical composition for treating epithelial covering

XX PT tissue comprises superstructure-forming nucleic acid sequences.

XX PS Disclosure; SEQ ID NO 12; 71pp; German.

XX CC This invention represents a novel cosmetic or pharmaceutical composition

CC for treating epithelial covering tissue which comprises superstructure-

CC forming nucleic acid sequences. The composition can also be used in

CC fabric softeners, hand-washing products, body and hair care products,

CC hair dyes or manual dishwashing products. The superstructures are G

CC quadruplexes, frayed wires or I motifs. The sequences are 30-40

CC nucleotides long, have five or more C, G or I nucleotides in tandem, no

CC CpG motifs, no nonmethylated CG dinucleotides, are polyI, polyC or polyG

CC homopolymers and are optionally modified by replacing phosphodiester

CC linkages with methyolphosphonate, phosphoramidate, phosphorothioate or

CC hydroxylamine linkages, by replaced ribose with other hexo- or

CC pentopyranoses or 3',5'-carbocyclically bridged 2'-deoxyribose

CC derivatives. The nucleic acid sequences are contained in liposomes. The

CC composition of the invention inhibits the release of IL-8. The

CC composition is useful for preventing or treating inflammatory changes to

CC epithelial covering tissue, including changes caused by pathogens,

CC autoimmune reactions, tumor necrosis factor, toxins and irritants,

CC especially aging processes, psoriasis, atopic eczema, dry skin, alopecia

CC areata, vitiligo, bullous diseases, rejection reactions, sunburn and

CC parodontosis. This sequence represents a phosphorothioate oligonucleotide

CC used to illustrate the method of the invention.

XX SQ Sequence 30 BP; 0 A; 30 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1..49e+05	Length:	30
Score:	53.00	Matches:	8
Percent Similarity:	80.0%	Conservative:	0
Best Local Similarity:	80.0%	Mismatches:	2
Query Match:	2.8%	Indels:	0
DB:	14	Gaps:	0

US-09-544-776-2 (1-373) x AEB28261 (1-30)

QY 139 ProProAlaArgProProProProProPro 148

Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 30

RESULT 8

ID AEC37003/c

AC AEC37003 standard; DNA; 30 BP.

XX AEC37003;

XX 03-NOV-2005 (first entry)

XX Phosphodiester oligodeoxyguanosine dG30.

XX Antimicrobial; antibacterial; fungicide; protozoasicide;

XX bacterial infection; fungal infection; protozoal infection; gene therapy;

XX drug screening; ss.

XX Synthetic.

XX WO2005079523-A2.

XX 01-SEP-2005.

XX 18-FEB-2005; 2005WO-US005398.

XX 18-FEB-2004; 2004US-0545370P.

XX 01-NOV-2004; 2004US-0623909P.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Evans DL, Kaur H, Jaso-Friedmann L, Leary JH, Praveen K;

XX WPI; 2005-582941/59.

XX New teleost-derived antimicrobial non-scavenger Receptor A, non-toll like

XX receptor polypeptide, useful for treating a disorder resulting from a

XX microbial infection and/or reducing antibiotic resistance.

XX Disclosure; SEQ ID NO 1; 84pp; English.

XX The invention provides an isolated antimicrobial non-scavenger receptor

XX A, non-toll like receptor polypeptide having a molecular weight of about

XX 22-30 kDa and having properties selected from: (a) (i) being obtainable

XX from a teleost, e.g. catfish (Ictalurus punctatus), mammalian monocytes

XX or mammalian macrophages, (ii) binds to oligoguanosine, (iii) comprises

XX 58 basic amino acids selected Lys and Arg, (iv) comprises 50 hydrophobic

XX amino acids selected from Ala, Ile, Leu, Phe, Trp and Val, and (v)

XX comprises 50 polar amino acids selected from Asn, Cys, Gln, Ser, Thr and

XX Tyr, containing 11 Lys-rich motifs; (b) comprises an amino acid sequence

XX selected from: amino acid residues 1-60, 1-118, 27-51, 136-159, or 173-

XX 203 of the catfish nonspecific cytotoxic cells antimicrobial protein-1

XX (NCAMP-1) AEC37005; (c) catfish NCAMP-1; (d) an allelic variant of

XX catfish NCAMP-1; (e) a polypeptide encoded by a nucleic acid molecule

XX that hybridizes under stringent conditions to the opposite strand of a

XX catfish NCAMP-1 nucleic acid molecule AEC37006; (f) catfish NCAMP-1

XX comprising conservative amino acid substitutions; and (g) a fragment of

XX (a)-(f) of at least 24 contiguous amino acids with antimicrobial

XX activity. A library comprising one or more of these polypeptides is

XX claimed. A method of identifying an antimicrobial polypeptide comprises

XX contacting candidate compounds with the polypeptide or library and

XX selecting those capable of inhibiting the bioactivity of the polypeptide.

XX The polypeptide is obtained by: optionally culturing cytotoxic cells from

XX a teleost fish, mammalian monocytes or mammalian macrophages; isolating

XX membranes from cultured cells consisting of NCs from a teleost fish;

XX isolating polypeptide from the isolated membranes; and determining if the

XX polypeptide binds to oligoguanosine and/or has antimicrobial activity.

XX Also claimed are nucleic acids encoding the antimicrobial polypeptide,

XX vectors and host cells, and a microarray comprising the nucleic acids. A

XX claimed method for detecting the presence or absence of an antimicrobial

XX polypeptide in a sample comprises determining the presence or absence of

XX a nucleic acid hybridizing to the catfish NCAMP-1 nucleic acid or

XX microarray, and assaying the sample for antimicrobial activity. Host

XX cells comprising the nucleic acid may be used to obtain the claimed

XX polypeptide. An antibody which binds the claimed polypeptide can also be

XX used to identify an antimicrobial protein. A claimed pharmaceutical

XX composition comprising the antimicrobial polypeptide and/or nucleic acid

XX is used to treat a disorder resulting from a microbial infection and/or

XX to reduce antibiotic resistance. The polypeptide is present in an amount

XX effective to inhibit microbial growth, e.g. bacterial, protozoa or fungal

XX growth in a subject, e.g. a mammal (human), or in an amount sufficient to

XX reduce antibiotic resistance. The present sequence is that of

XX phosphodiester oligodeoxyguanosine Po dG30. Pretreatment of J774 cells

XX with Po dG30 has been shown to inhibit Escherichia coli DNA,

US-09-544-776-2 (1-373) x ABK95215 (1-30)

QY 139 ProProAlaArgProProProProProPro 148
 Db 1 CCACCTCCACCTCCACCTCCACCTCCACCT 30

RESULT 11

ABK95215/c
 ID ABK95215 standard; DNA; 28 BP.

AC ABK95215;

DT 24-SEP-2002 (first entry)

XX PCR primer containing part of c-jun and 8 repeated His-tags.

DE C-terminal modified protein; protein interaction detection;

XX C-terminal modified protein; protein interaction detection; PCR; primer; ss.

KW proteome analysis; protein-nucleic acid interaction; PCR; primer; ss.

XX Synthetic.

OS WO200246395-A1.

PN 13-JUN-2002.

PD 07-DEC-2001; 2001WO-JP010731.

PF 07-DEC-2000; 2000JP-00373105.

PR (UYKE-) UNIV KEIO.

PA Yanagawa H, Doi N, Miyamoto E, Takashima H, Oyama R;

PI WPI; 2002-500446/53.

PT Production of C-terminal modified proteins with nucleotide-linker
 PT containing modifying agents and translation templates, useful for
 PT detecting protein interaction in functional analysis of genes e.g. in
 PT genome projects.

XX Example 5; Page 88; 95pp; Japanese.

XX The invention relates to an agent for modifying the C-terminal of a
 CC protein comprising an acceptor region with a group capable of binding to
 CC a protein through a transpeptidation reaction in a protein translation
 CC system, and a modifying region containing a non-radioactive modifier
 CC linked to a part of the acceptor region via a nucleotide linker. The
 CC modified proteins are useful for detecting protein interaction in
 CC functional analysis of genes e.g. in genome projects, as well as protein-
 CC nucleic acid interaction in large quantities in high-throughput screening
 CC when studying biological molecules such as proteins and nucleic acids in
 CC genome function or proteome analysis. The modified proteins can be
 CC conveniently and quickly applied in studying protein interactions, with
 CC improved efficiency. ABK95189-ABK95225 represent PCR primers used in
 CC examples of the invention

XX Sequence 28 BP; 0 A; 1 C; 17 G; 10 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.9e+05	Length:	28
Score:	50.00	Matches:	9
Percent Similarity:	81.8%	Conservative:	0
Best Local Similarity:	81.8%	Mismatches:	0
Query Match:	2.6%	Indels:	2
DB:	6	Gaps:	1

US-09-544-776-2 (1-373) x ABK95215 (1-28)

QY 138 GluProAlaArgProProProProProPro 148

Db 28 GAACACCA-----CCACACACACACACCA 2

RESULT 12

ABN81202/c
 ID ABN81202 standard; DNA; 30 BP.

XX AC ABN81202;

XX 06-AUG-2003 (revised)

DT 16-JUL-2002 (first entry)

XX Litopenaeus vannamei microsatellite detection probe 2.

DE Giant black tiger prawn; Penaeus monodon; pacific white shrimp;

XX Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;

XX Taura Syndrome Virus; TSV; infection; probe; ss.

XX Litopenaeus vannamei.

OS Synthetic.

PN WO200034476-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99WO-US029571.

XX 10-DEC-1998; 98US-0111670P.

XX (TUFT) TUFTS COLLEGE.

PA Alcivar-Warren A, Xu Z, Dhar AK, Fan Y, Meehan D, Garcia DK;

PI WPI; 2000-423422/36.

XX Polynucleotides of shrimp are useful for identifying, mapping and
 PT characterizing of the genome of various species of shrimp.

XX Page 60; Example 4; 120pp; English.

XX The invention relates to an isolated polynucleotide (I) of the giant
 CC black tiger prawn, Penaeus monodon or expressed sequence tags of the
 CC pacific white shrimp, Litopenaeus vannamei (ABN80997-ABN81172), both
 CC containing microsatellites sequences including those P. monodon
 CC microsatellite sequence given in GenBank AF077550-AF077598. (I), the
 CC complementary sequence or fragment and the encoded polypeptide are useful
 CC for mapping of the genome of various species of shrimp. Mapping the
 CC genome of Penaeus is useful for determining whether a test shrimp,
 CC preferably Litopenaeus vannamei, has a genotype associated with a
 CC phenotypic trait such as resistance to Taura Syndrome Virus (TSV)
 CC infection. The present sequence is that of a probe, useful in examples of
 CC the invention. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 30 BP; 0 A; 20 C; 0 G; 10 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.02e+05	Length:	30
Score:	50.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	2.6%	Indels:	0
DB:	3	Gaps:	0

US-09-544-776-2 (1-373) x ABN81202 (1-30)

QY 34 GluGluGluGluGluGluGluGluGlu 43

Db 30 GAGGAGGAGGAGGAGGAGGAGGAGGAG 1

RESULT 13

ABZ22047

ID ABZ22047 standard; DNA; 30 BP.

XX AC ABZ22047;

XX 11-MAR-2003 (first entry)

XX

QY 34 GluGluGluGluGluGluGluGluGluGlu 43
 |||||
 DB 30 GAGGAAGAGAGAGAGAGAGAGAGAGAA 1

RESULT 15
 ABZ22086
 ID ABZ22086 standard; DNA; 30 BP.
 XX
 AC ABZ22086;
 XX

XX 11-MAR-2003 (first entry)
 XX
 DE Polyanionic polymer related oligonucleotide #40.
 XX
 XX Polyanionic polymer; bioactivity; water solubility; ss.
 KW
 XX Synthetic.
 OS
 XX WO200277036-A2.
 PN
 XX 03-OCT-2002.
 PD
 XX 21-MAR-2002; 2002WO-US008614.
 PF
 XX 21-MAR-2001; 2001US-0277705P.
 PR
 XX (LEUNG/) LEUNG D W.
 PA

PI Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;
 PI Waggoner DW;
 XX
 XX WPI; 2003-058367/05.

XX Producing monodispersed preparation of polyanionic polymer for therapy,
 PT by expressing vector comprising ligation product of oligonucleotides
 PT encoding glutamate/aspartate residues in host cell and isolating the
 PT product.
 PT
 XX

PS Example 1; Fig 2; 74pp; English.

XX The present invention describes a method (M) for producing a
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
 CC kD. (M) involves inserting into an expression vector (EV) a ligation
 CC product formed by ligating together oligonucleotides that encode
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
 CC approximately of the same molecular weight. Also described: (1) a
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
 CC another polypeptide at either one end or at both ends of it; (2) a
 CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
 CC Leukine, where the polyanionic polymer is polyglutamic acid or
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at
 CC least one other nucleotide sequence, where the polyanionic polymer is
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
 CC (IV) comprising (III) or a vector that comprises a nucleotide sequence
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
 CC is useful for treating a disease or ailment in an individual by
 CC administering (I) to the individual. (I) is also useful for delivering an
 CC effective amount of a pharmaceutically active agent, a therapeutic
 CC protein or a drug to a patient in need of it, or for diagnostic and
 CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to
 CC ABP56400 represent sequences used in the exemplification of the present
 CC invention
 XX

SQ Sequence 30 BP; 16 A; 0 C; 14 G; 0 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.02e+05 Length: 30
 Score: 50.00 Matches: 10
 Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 2.6% Indels: 0
 DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x ABZ22086 (1-30)

QY 34 GluGluGluGluGluGluGluGluGluGlu 43
 |||||
 DB 1 GAAGAGGAAGAGAGAGAGAGAGAGAGAG 30

RESULT 16
 AAL43651/c
 ID AAL43651 standard; DNA; 28 BP.
 XX
 AC AAL43651;
 XX

XX 05-SEP-2002 (first entry)
 XX
 DE Human telomerase catalytic subunit (HTE RT) PCR primer OVT1561.
 XX
 KW Human; protein-ligand interaction; PCR; primer; ss; OVT1561; HTE RT;
 KW perturbation library; target molecule identification; drug development;
 KW telomerase catalytic subunit.
 XX
 OS Homo sapiens.
 XX
 XX US2002045188-A1.
 PN
 XX 18-APR-2002.
 PD
 XX 25-MAY-2001; 2001US-00865644.
 PF
 XX 17-NOV-1998; 98US-00193759.
 PR
 XX 17-NOV-1999; 99WO-US027409.
 XX

XX (KAMB/) KAMB C A.
 PA (CAPO/) CAPONIGRO G M.
 PA (TENG/) TENG D H.
 PA (SAND/) SANDROCK T M.
 PA (STUM/) STUMP M.
 XX

XX Kamb CA, Caponigro GM, Teng DH, Sandrock TM, Stump M;
 PI WPI; 2002-507237/54.
 XX

XX A new method for identifying a physiological target molecule that
 PT correlates to a phenotype of interest involves using a library of
 PT putative perturbation probes against target molecules, and is useful in
 PT drug development.

XX Example 10; Page 20; 37pp; English.

XX The invention comprises a method for identifying a physiologically
 CC relevant target molecule that correlates to a phenotype of interest. The
 CC method involves determining protein-ligand interactions between a target
 CC candidate and a library of perturbagens and performing a phenotypic assay
 CC to determine physiologically relevant perturbagens. The method of the
 CC invention results in fewer false positive results than prior art methods
 CC and can be used in drug development. The present DNA sequence represents
 CC a PCR primer used to amplify the gene sequence of the human telomerase
 CC catalytic subunit (HTE RT)

XX Sequence 28 BP; 3 A; 4 C; 21 G; 0 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.1e+05 Length: 28
 Score: 49.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 2
 Best Local Similarity: 77.8% Mismatches: 0
 Query Match: 2.6% Indels: 0
 DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x AAL43651 (1-28)

Qy 142 ArgProProProProProProAlaSer 150
ID ADP17616 standard; DNA; 25 BP.
Db 27 CGCCCGCGCGCGCCCTCTTCGCC 1

RESULT 17
ADP17616
AC ADP17616;
AC ADP17616;
DT 26-AUG-2004 (first entry)
DE Renal cell carcinoma differentially expressed gene probe #4021.
DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
XX WO2004048933-A2.
XX
XX 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 4352; 350pp; English.

CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.

SQ Sequence 25 BP; 3 A; 4 C; 8 G; 10 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 2.33e+05 Length: 25
Score: 47.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 2.5% Indels: 0
DB: 12 Gaps: 0
US-09-544-776-2 (1-373) x ADP17616 (1-25)

Qy 307 TrpValPheThrTyrValGlyAla 314
Db 2 TGGGTATTACCTATGTTGGTCC 25

RESULT 18
AAT09304
ID AAT09304 standard; DNA; 30 BP.
XX
AC AAT09304;
XX
XX 25-JUL-1996 (first entry)
DE Murine anti-Protein C Mab HPC-4 VH and VL variable region primer.
XX
XX Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
KW zymogen; cleavage; mouse; humanised antibody; variable region;
KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
XX
XX Synthetic.
XX
XX WO9534652-A1.
XX
XX 21-DEC-1995.
XX
XX 09-JUN-1995; 95WO-US007372.
XX
XX 10-JUN-1994; 94US-00259321.
XX
XX (OKLA-) OKLAHOMA MED RES FOUND.
XX
XX Rezaie A, Esmon CT;
XX WPI; 1996-049681/05.
XX
XX Calcium-binding monoclonal antibody immunoreactive with Protein C -
PT inhibits Protein C anticoagulant activation by thrombin-thrombomodulin,
PT e.g. for treating tumours.
XX
XX Disclosure; Page 10; 41pp; English.

CC The primers AAT09303-4 were used to amplify sequence encoding the heavy
CC chain variable region from the murine anti-protein C monoclonal antibody
CC HPC-4, using a first strand cDNA as template. This primer consists of a
CC poly(dC) tail which matches the poly(dG) tail added to the first cDNA.
CC With primer AAT09305, this primer was used to amplify the encoding the
CC HPC-4 light chain variable region. HPC-4 recognises the activation
CC peptide region (AAR88106) of the heavy chain of protein C, a vitamin K-
CC dependent plasma protein zymogen. Protein C is converted to activated
CC protein C (APC) by cleavage between the Arg-leu amino acid contained
CC within the activation peptide sequence. HPC-4 prevents protein C
CC activation to APC by binding to this region. The DNA sequences encoding
CC the variable regions of the heavy and light chains of the antibody
CC (AAT09299-302) were used to construct humanised antibodies using the PCR
CC primers AAT09303-5. The humanised antibodies are useful as inhibitors of
CC coagulation and can be used for the treatment of tumours by inhibiting
CC the anticoagulant activity of APC by preventing conversion of protein C
CC to APC
XX
XX Sequence 30 BP; 2 A; 24 C; 4 G; 0 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 2.74e+05 Length: 30
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 2 Gaps: 0

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US-09-544-776-2 (1-373) x AAT09304 (1-30)
QY 142 ArgProProProProPro 148
DB 4 CGCGCGCGCGCGCGCGCGCGCG 24

RESULT 19
AAA74323
ID AAA74323 standard; DNA; 30 BP.
AC AAA74323;
XX
DT 29-NOV-2000 (first entry)
XX
DE Loblolly pine SSR repeat of locus RIPPT2.
XX
KW Loblolly pine; Simple Sequence Repeat; SSR; microsatellite DNA repeat;
KW genetic marker; mapping; inheritance study; population genetics study;
KW plant breeding programme; ss.
XX
OS Pinus taeda.
XX
PN WO200042210-A2.
XX
PD 20-JUL-2000.
XX
PF 06-JAN-2000; 2000WO-US000325.
XX
PR 15-JAN-1999; 99US-00232884.
PR 19-JAN-1999; 99US-00232785.
XX
PA (INTO ) INT PAPER CO.
PA (ECHR/) ECHT C S.
PA (NELS/) NELSON C D.
PA (USDA ) US SEC OF AGRIC.
XX
XX Echt CS, Nelson CD;
PI WPI; 2000-482836/42.
XX
XX Polynucleotide having simple sequence repeat useful as markers in plants
PT for genetic characterization e.g. genetic mapping study, an inheritance
PT study of a commercially important trait in a plant breeding program.
XX
PS Example; Page 49; 57pp; English.
XX
CC The present invention relates to loblolly pine polynucleotides with one
CC or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). The present
CC sequence is one such SSR repeat. SSRs are also known as microsatellite
CC DNA repeats. The SSRs are useful as genetic markers for genetic mapping,
CC population genetics studies and inheritance studies in various plant
CC breeding programmes
XX
SQ Sequence 30 BP; 10 A; 16 C; 0 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.74e+05 Length: 30
Score: 47.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 2.5% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x AAA74323 (1-30)
QY 143 ProProProProProProPro 150
DB 2 CCACCACCACCACCACCACCATCA 25

RESULT 20
AED96668/C
ID AED96668 standard; DNA; 24 BP.
XX

```

```

AC AED96668;
XX
DT 26-JAN-2006 (first entry)
XX
DE Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 847.
XX
KW Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antiinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
KW cerebrovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
KW C-reactive protein pentraxin-related; CRP; genetic marker; da.
XX
OS Homo sapiens.
XX
PN WO2005107364-A2.
XX
PD 17-NOV-2005.
XX
PF 27-JAN-2005; 2005WO-IB002407.
XX
PR 27-JAN-2004; 2004US-0539128P.
PR 27-JAN-2004; 2004US-0539129P.
PR 22-OCT-2004; 2004US-0620874P.
PR 22-OCT-2004; 2004US-0621004P.
PR 25-OCT-2004; 2004US-0621053P.
PR 25-OCT-2004; 2004US-0621072P.
PR 26-OCT-2004; 2004US-0621663P.
PR 27-OCT-2004; 2004US-0622016P.
PR 27-OCT-2004; 2004US-0622017P.
PR 27-OCT-2004; 2004US-0622320P.
PR 17-NOV-2004; 2004US-0628101P.
PR 17-NOV-2004; 2004US-0628112P.
PR 17-NOV-2004; 2004US-0628133P.
PR 17-NOV-2004; 2004US-0628134P.
PR 17-NOV-2004; 2004US-0628144P.
PR 17-NOV-2004; 2004US-0628145P.
PR 17-NOV-2004; 2004US-0628156P.
PR 17-NOV-2004; 2004US-0628165P.
PR 17-NOV-2004; 2004US-0628179P.
PR 17-NOV-2004; 2004US-0628190P.
PR 17-NOV-2004; 2004US-0628231P.
PR 17-NOV-2004; 2004US-0628251P.
PR 26-NOV-2004; 2004US-0630559P.
PR 08-DEC-2004; 2004US-0634075P.
PR 27-JAN-2005; 2005US-00043806.
XX
XX (COMP-) COMPUGEN LTD.
XX (COHE/) COHEN Y.
XX
PI Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocaru GS;
PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX
XX WPI; 2005-810779/82.
XX
XX New polynucleotide, useful for diagnosing a CRP variant-detectable
PT disease or for selecting therapy for a CRP variant-detectable disease,
PT e.g., myocardial infarction, coronary artery disease.
XX
XX Disclosure; SEQ ID NO 847; 1670pp; English.
XX
CC The invention relates to a new isolated polynucleotide. The
CC polynucleotide is useful for diagnosing a CRP variant-detectable disease,
CC for monitoring disease progression or treatment efficacy or relapse of a
CC CRP variant-detectable disease or for selecting therapy for a CRP variant
CC -detectable disease, e.g., myocardial infarction, coronary artery
CC disease, non-fatal or fatal stroke, peripheral vascular disease,
CC congestive heart failure or sudden cardiac death. The present sequence
CC represents a human C-reactive protein, pentraxin-related (CRP) associated
CC marker DNA.
XX
SQ Sequence 24 BP; 1 A; 2 C; 20 G; 1 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 2.48e+05 Length: 24
Score: 46.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.4% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x AED96668 (1-24)

Qy 143 ProProAlaArgProProPro 149
Db 22 CCCCCCCCCCCCCCCCCCTGCA 2

RESULT 21

AAQ40855
ID AAQ40855 standard; DNA; 27 BP.

XX AC AAQ40855;

XX DT 23-SEP-1993 (first entry)

XX DE DNA sequence used in DNA replication method.

XX KW ss.

XX OS Synthetic.

XX PN JP05103673-A.

XX PD 27-APR-1993.

XX PF 26-AUG-1991; 91JP-00240525.

XX PR 26-AUG-1991; 91JP-00240525.

XX PA (UYAR-) UNIV ARIZONA.

XX DR WPI; 1993-171830/21.

XX PT Replication of DNA - useful in genetic engineering and medical applications.

XX PS Disclosure; Page 20; 20pp; Japanese.

XX CC The sequence is given in the disclosure to illustrate the invention

XX SQ Sequence 27 BP; 0 A; 27 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.76e+05 Length: 27
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAQ40855 (1-27)

Qy 139 ProProAlaArgProProProPro 147
Db 1 CCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 22

AAQ40856/c
ID AAQ40856 standard; DNA; 27 BP.

XX AC AAQ40856;

XX DT 23-SEP-1993 (first entry)

XX DE DNA sequence used in DNA replication method.

XX KW ss.
XX OS Synthetic.
XX PN JP05103673-A.
XX PD 27-APR-1993.
XX PF 26-AUG-1991; 91JP-00240525.
XX PR 26-AUG-1991; 91JP-00240525.
XX PA (UYAR-) UNIV ARIZONA.
XX DR WPI; 1993-171830/21.
XX PT Replication of DNA - useful in genetic engineering and medical applications.
XX PS Disclosure; Page 20; 20pp; Japanese.
XX CC The sequence is given in the disclosure to illustrate the invention

XX SQ Sequence 27 BP; 0 A; 0 C; 27 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.76e+05 Length: 27
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAQ40856 (1-27)

Qy 139 ProProAlaArgProProProPro 147
Db 27 CCCCCCCCCCCCCCCCCCCCCCCC 1

RESULT 23

ADV96473/c
ID ADV96473 standard; DNA; 27 BP.

XX AC ADV96473;

XX DT 07-APR-2005 (first entry)

XX DE CGG repeat region of DNA sequence.

XX KW Microbial typing; genetic marker; DNA typing; diagnosis; repetitive DNA;
XX KW DNA ligation; luminescence; Fragile X syndrome; Huntingtons chorea;
XX KW dystrophy; ataxia; SNP detection; genetic disorder; ds;
XX OS variable tandem repeat polymorphism.

XX XH Homo sapiens.

XX FT Key Location/Qualifiers
XX FT repeat_region 1..27 /*tag= b
XX FT /rpt_type= TANDEM
XX FT /note= "9 CGG codons"
XX FT repeat_unit 1..3
XX FT /*tag= a
XX FT /function= "CGG codon"

XX WO2005003386-A2.

XX PN 13-JAN-2005.

XX PF 30-JUN-2004; 2004WO-EP007090.

XX PR 30-JUN-2003; 2003SE-00001951.

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PR 30-JUN-2003; 2003US-0481043P.
PR 01-SEP-2003; 2003US-0481319P.
XX (BIOT-) BIOTAGE AB.
XX Tooke N, Ekstroem B;
XX WPI; 2005-101504/11.
XX
XX Determining the presence of genetic element(s), e.g. nucleotide
XX repeat(s), or marker(s) for microbial typing, in a nucleic acid sample,
XX useful in diagnostic methods, by performing a ligation reaction and
XX detecting a ligation by-product.
XX
XX Disclosure; SEQ ID NO 5; 53pp; English.
XX
XX The present invention relates to estimating the number of nucleotide
XX repeats and determining the presence of other genetic element(s), such as
XX marker(s) for microbial typing, by ligating the oligonucleotide(s)
XX annealed to the nucleic acid sample to each other using a ligase enzyme
XX and detecting a ligation-by-product to determine whether a ligation
XX reaction has occurred. Specifically, analyzing the number of repeats in a
XX sample comprises providing a nucleic acid sample potentially comprising a
XX repeat; providing oligonucleotide(s) complementary to the repeat;
XX annealing the oligonucleotide(s); ligating the oligonucleotide(s)
XX annealed to the nucleic acid sample to each other using a ligase enzyme;
XX converting a ligation by-product into ATP; and detecting the ATP by a
XX luciferase-based assay to determine whether a ligation reaction has
XX occurred. One of the oligonucleotides is adapted to anneal immediately
XX outside the repeated sequence. The oligonucleotide employed is a mono-,
XX di- or multimer of the repeat in itself. The oligonucleotides are
XX complementary to, but that are out of phase with, the repeat. Unannealed
XX oligonucleotides are removed after the detection by using an exonuclease,
XX and are inactivated after the detection by using a phosphatase.
XX Oligonucleotides are complementary to a genetic region, optionally with
XX an AopP5' modification, that is informative for identification of
XX microbial species, from the following groups: 16S rRNA gene, 23S rRNA
XX gene, groEL, gyrB, rpoB, rnpB and groEL, microsatellite and
XX minisatellite, VNTRs, the nuclear ribosomal DNA (rDNA) array - small-
XX subunit (SSU) (18S-like), large-subunit (LSU) (23S, 26S, or 28S-like),
XX 5.8S rRNA genes, and internal transcribed ribosomal DNA (rDNA) spacers
XX (ITS1 and ITS2). The method is useful in diagnosing dentatorubral
XX pallidoluysian atrophy (DRPLA), Fragile X syndrome, Fragile site FRAXE,
XX Huntington's disease, Kennedy's disease, Machado-Joseph disease, Myotonic
XX dystrophy, Friedrich's ataxia, and spinocerebellar ataxia. The present
XX sequence is a DNA sequence comprising CCG repeats useful for detection of
XX fragile X syndrome.
XX
XX Sequence 27 BP; 0 A; 9 C; 18 G; 0 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,76e+05 Length: 27
XX Score: 46.00 Matches: 7
XX Percent Similarity: 77.8% Conservative: 0
XX Best Local Similarity: 77.8% Mismatches: 2
XX Query Match: 2.4% Indels: 0
XX DB: 14 Gaps: 0
XX
XX US-09-544-776-2 (1-373) x ADV96473 (1-27)
XX
XX QY 139 ProProAlaArgProProProProPro 147
XX
XX Db 27 CCGCGCGCGCGCGCGCGCGCGCGCGCG 1
XX
XX RESULT 24
XX AAQ41910/c
XX ID AAQ41910 standard; DNA; 28 BP.
XX
XX AC AAQ41910;
XX
XX DT 25-MAR-2003 (revised)
XX DT 30-SEP-1993 (first entry)
XX

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```

DE erb B2/neu promoter parallel TFO #3.
XX Purine; promoter; human; erb B2/neu; gene; HER-2; homologue; rat; neu;
XX triplex-forming oligonucleotide; TFO; retinoic acid; transgenic mice;
XX core promoter element; growth factor; c-AMP; cancer; mammary tumour;
XX tumour; NIH3T3 cells; pyrimidine; TPA; major groove; target; CAT box;
XX TATA box; transcription; transforming; AT box protein; RNA polymerase;
XX TFIIId; control isomer; expression; ss.
XX
XX Synthetic.
XX OS
XX WO9309788-A1.
XX
XX 27-MAY-1993.
XX
XX 28-OCT-1992; 92WO-US009202.
XX
XX 13-NOV-1991; 91US-00792319.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Hogan ME;
XX
XX WPI; 1993-182231/22.
XX
XX Use of triplex-forming oligo-nucleotide - to inhibit proliferation of
XX cells contg. an erb. B2/neu gene site, for treating cancers, psoriasis
XX etc.
XX
XX Claim 14; Page 17; 26pp; English.
XX
XX The sequences given in AAQ41905-10 are triplex-forming oligonucleotides
XX (TFO) which are specific to the promoter region of erb B2/neu. They bind
XX to the major groove of the DNA duplex to form a triplex. The TFOs are
XX complementary to the target sequence such they include a G when the
XX complementary location in the DNA duplex is a GC pair and T when the
XX complementary location in the DNA duplex is an AT base pair. The target
XX site for these TFOs should have a stretch of DNA which is at least 65%
XX purine or pyrimidine bases. The long purine run in the erb B2/neu
XX promoter region includes the CAT box and the TATA box. Inhibition at the
XX CAT box will inhibit transcription initiation by interfering directly
XX with the CAT box protein-RNA polymerase interaction. Further inhibition
XX of the protein binding at the CAT box site can also block the interaction
XX of the CAT protein with TFIIId at the TATA box. The sequences given in
XX AAQ41911-13 are control isomers which comprise randomised sequences based
XX on TFOs which do not bind to the erb B2/neu target sequence, and have no
XX effect on erb B2/neu expression. The erb B2/neu (HER-2) gene is the human
XX homologue of the rat neu gene. This human homologue is frequently
XX amplified in tumours. When expressed at high levels in NIH3T3 cells, erb
XX B2/neu is strongly transforming and results in a high incidence of erb
XX mammary tumours in transgenic mice. The core promoter element of erb
XX B2/neu resides within a 300 bp region of the 5' flanking domain. This
XX region contains elements which confer sensitivity to enhance promoter
XX function in the presence of cell growth factors such as TPA, c-AMP and
XX retinoic acid. Therefore, overexpression of erb B2/neu may be one
XX mechanism leading to cancer initiation or expression. Inhibition of the
XX erb B2/neu promoter region by the TFOs may be used to inhibit expression
XX of the gene and may therefore be used to treat or prevent cancers.
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 28 BP; 0 A; 0 C; 18 G; 10 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,85e+05 Length: 28
XX Score: 46.00 Matches: 7
XX Percent Similarity: 77.8% Conservative: 0
XX Best Local Similarity: 77.8% Mismatches: 2
XX Query Match: 2.4% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-544-776-2 (1-373) x AAQ41910 (1-28)
XX
XX QY 140 ProAlaArgProProProProPro 148
XX

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```
Db      27  CCACCAACCACCACCACCACCACC 1
RESULT 25
AAQ88043
ID      AAQ88043 standard; RNA; 28 BP.
XX
AC      AAQ88043;
XX
DT      25-MAR-2003 (revised)
DT      31-OCT-1995 (first entry)
XX
XX      CU-rich triplex binding motif for HER2 promoter fragment.
DE
XX      HER2 promoter; triplex RNA; binding motif; ss.
KW
XX      Synthetic.
OS
XX      WO9510607-A1.
PN
XX
PD      20-APR-1995.
XX
PF      14-OCT-1994; 94WO-US011616.
XX
PR      14-OCT-1993; 93US-00138666.
XX
XX      (REGC ) UNIV CALIFORNIA.
PA
XX      Noonberg SH, Hunt AC;
PI
XX      WPI; 1995-161794/21.
XX
XX      Constructs having 5'-stabilising and 3'-terminating flanking regions, -
PT      for intracellular generation of oligo:nucleotide transcript, useful in
PT      gene regulation and therapy.
XX
XX      Example; Fig 3; 145pp; English.
PS
XX
XX      AAQ88045 is a ds probe which corresp. to bases -68 to -19 on the HER2/c-
CC      erb B2/neu proto-oncogene. It contains a homopurine/homopyrimidine tract
CC      involved in triplex formation. The CU-rich (AAQ88043) and GA-rich
CC      (AAQ88044) RNA sequences corresp. to pyrimidine (parallel) or purine
CC      (antiparallel) third strand triplex binding motifs respectively. The CU-
CC      rich RNA was generated in vitro from a pBluescript deriv. in which the
CC      multicloning site was replaced with a 28 bp synthetic oligo duplex. When
CC      linearised with SstI and transcribed by T3 RNA polymerase the transcript
CC      AAQ88043 was generated. When linearised with KpnI and transcribed by T7
CC      RNA polymerase in the opposite orientation, the corresp. antisense GA-
CC      rich strand was generated. Both transcripts also contained approx. 12 nts
CC      of flanking RNA derived from cloning and the polymerase start sequences.
XX      (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 28 BP; 0 A; 19 C; 0 G; 0 T; 9 U; 0 Other;

Alignment Scores:
Pred. No.:      2.85e+05      Length:      28
Score:          46.00      Matches:      7
Percent Similarity: 77.8%      Conservative: 0
Best Local Similarity: 77.8%      Mismatches: 2
Query Match:    2.4%      Indels:      0
DB:            2      Gaps:        0

US-09-544-776-2 (1-373) x AAQ88043 (1-28)

QY      140 ProAlaArgProProProProPro 148
      ||| ||||| ||||| ||||| |||||
Db      2 CCUCUCCUCCUCCUCCUCCUCC 28

RESULT 26
AAV08947/c
ID      AAV08947 standard; cDNA; 28 BP.
XX
XX      AAV08947;
AC
```

```
XX      01-MAR-1999 (first entry)
XX      PCR primer for Human ATG-1709 protein coding sequence.
DE
XX      Human; ATG-1709 protein; secreted ligand; 7-Transmembrane receptor;
KW      heart disease; hypertension; cardiovascular disease; kidney disease;
KW      obesity; insulin resistance; diabetes; Central Nervous System disorder;
KW      therapy; SPRP-1; PCR primer; ss.
XX
XX      Synthetic.
OS      Homo sapiens.
XX      EP879885-A1.
PN
XX      25-NOV-1998.
XX
XX      16-JAN-1998; 98EP-00300313.
XX      23-MAY-1997; 97US-0047691P.
XX      08-AUG-1997; 97US-00907808.
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
PA
XX      Hu E, Zhu Y;
PI
XX      WPI; 1998-596877/51.
XX
XX      New human secreted protein ATG-1709 polypeptide and polynucleotide -
PT      useful as diagnostic reagents and for diagnosing, prevention and
PT      treatment of Central Nervous System diseases and diabetes.
XX
XX      Example 1; Page 13; 28pp; English.
XX
XX      This sequence is a PCR primer for DNA encoding the human ATG-1709 protein
CC      of the invention. ATG-1709 is related to human secreted ligands for 7-
CC      Transmembrane receptors and similar to murine SPRP-1. ATG-1709
CC      polypeptides and polynucleotides are useful for diagnosing susceptibility
CC      to diseases by detecting mutations in the ATG-1709 gene using probes
CC      containing the ATG-1709 nucleotide sequence, and can diagnose diseases
CC      associated with ATG-1709 imbalance by determining ATG-1709 polypeptide
CC      expression levels. ATG-1709 polypeptides can be used to screen for
CC      agonists and antagonists which bind the ATG-1709 polypeptide. These can
CC      be used in treatment to activate or inhibit ATG-1709 activity, in
CC      addition to direct administration of antisense sequences to prevent
CC      expression, or ATG-1709 polypeptides to treat conditions associated with
CC      a lack of ATG-1709. Gene therapy may also be used to affect endogenous
CC      ATG-1709 expression. ATG-1709 antibodies are useful for inducing an
CC      immune response to immunise and prevent diseases, and for isolating ATG-
CC      1709 clones or purifying the polypeptides by affinity chromatography. ATG
CC      -1709 polypeptides can be administered directly or as a vaccine to
CC      inoculate against disease. Diseases diagnosed, prevented or treated
CC      include: heart disease; hypertension; cardiovascular diseases; kidney
CC      diseases; obesity; insulin resistance; diabetes and Central Nervous
CC      System (CNS) diseases. The ATG-1709 polypeptide is also useful for
CC      mapping the gene to a chromosome, allowing gene inheritance to be studied
CC      through linkage analysis
XX
SQ      Sequence 28 BP; 3 A; 7 C; 15 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      2.85e+05      Length:      28
Score:          46.00      Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    2.4%      Indels:      0
DB:            2      Gaps:        0

US-09-544-776-2 (1-373) x AAV08947 (1-28)

QY      143 ProProProProProProPro 149
      ||| ||||| ||||| ||||| |||||
Db      28 CCGCCGCGCGCGCGCGCGCGCA 8
```

```

RESULT 27
AAV02972
ID AAV02972 standard; cDNA; 28 BP.
XX
AC AAV02972;
XX
DT 11-MAY-1998 (first entry)
XX
DE Hepatitis GB virus (HGV) type C gene PCR primer GBC-14.
XX
KW Hepatitis GB virus type C; HGV: GBV-C gene; nonB nonC Hepatitis virus;
KW detection; hybridise; PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis virus.
XX
PN JP10004971-A.
XX
PD 13-JAN-1998.
XX
PF 25-JUN-1996; 96JP-00164443.
XX
PR 25-JUN-1996; 96JP-00164443.
XX
PA (TOFU ) TONEN CORP.
XX
WPI; 1998-133626/13.
XX
DR Method for detecting the GBV-C gene - using an oligonucleotide in high
PT sensitivity assay.
XX
PS Example 2; Page 11; 11pp; Japanese.
XX
CC PCR primers AAV02959-V02977 are used to amplify fragments of the
CC Hepatitis GB virus (HGV) type C gene isolated from the serum of nonB nonC
CC chronic hepatitis patients. These fragments are used in devising a highly
CC sensitive method for the detection of the GBV-C gene using an
CC oligonucleotide which can hybridise with any of these GBV-fragments
XX
SQ Sequence 28 BP; 7 A; 15 C; 2 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAV02972 (1-28)

QY 140 ProAlaArgProProProPro 147
Db 5 CCTCAACGACCTCTCCACCA 28

RESULT 28
AAV44665/c
ID AAV44665 standard; DNA; 28 BP.
XX
AC AAV44665;
XX
DT 07-OCT-1998 (first entry)
XX
DE Triplex-forming oligonucleotide HN28ap.
XX
KW Triplex-forming oligonucleotide; her-2/neu promoter; HN28ap; HN28apPTE;
KW polycationic oligomer; nucleic acid uptake; gene therapy;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers

```

```

FT modified_base 1. .28
FT /*tag= a
XX /mod_base= optionally phosphorothioate ester backbone
XX
PN WO9827209-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US024253.
XX
PR 18-DEC-1996; 96US-0032436P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Liotta DC, Petros JA, Mey S, Karr JF, Pohl J;
XX WPI; 1998-362778/31.
XX
PT New polycationic oligomer cell transfection agent(s) - are size-selected
PT for precise neutralisation of nucleic acid charge to facilitate uptake in
PT e.g. cancer cells.
XX
PS Claim 85; Page 81; 91pp; English.
XX
CC This sequence represents the triplex forming oligonucleotide HN28ap (the
CC phosphorothioate ester form is known as HN28apPTE), which targets the her
CC -2/neu promoter. This sequence can be used with the polycationic
CC oligomers of the invention. The polycationic oligomers are of discrete
CC length, and have a repeating structure of formula (I): [(REP)m-(M) r-
CC (REP)n-(M)el1-(REP)p (I); M = flexible spacer; r,s = 0 or 1; m,n,p,l =
CC the numbers of corresponding units, where the total number of repeating
CC units (z) in (I) is 1(m + n) + p; REP = repeating unit containing a
CC cationic side-group (CSG) and having the structure -[X1-Q1-CO-Y2-Q2-CO]-;
CC Y1 = O or NR3; Y2 = O or NR4; one of Q1 and Q2 in each repeating unit =
CC (CH2)w and the other = CHR'; w = 1-3; R',R3,R4 = H, 1-3C alkyl, a non-
CC cationic side-group or a CSG, provided that one, and only one, CSG is
CC present in each repeating unit. The polycationic oligomers are useful as
CC transfecting agents for facilitating the uptake of nucleic acids into
CC eukaryotic cells in vitro or in vivo, especially human cells, e.g. in
CC research, diagnostics or gene therapy. The polycationic oligomer is
CC especially used in the transfection of cancer cells, e.g. for the gene
CC therapy treatment of prostate cancer by introduction of this sequence.
CC The polycationic oligomer/nucleic acid complexes can be administered in
CC pharmaceutical compositions. The size of the polycationic oligomers can
CC be selected to neutralise the charge of a specific nucleic acid precisely
CC and thus facilitate its uptake. The oligomers can also be designed to
CC have varying degrees of biodegradability or to contain a wide range of
CC biological active moieties, e.g. for targeting or labelling
XX
SQ Sequence 28 BP; 8 A; 0 C; 19 G; 1 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAV44665 (1-28)

QY 139 ProProAlaArgProProProPro 147
Db 27 CCTCCTCCTCCTCCACCTCTCTCTCC 1

RESULT 29
AAF99570
ID AAF99570 standard; DNA; 28 BP.
XX
AC AAF99570;
XX
DT 12-JUN-2001 (first entry)
XX

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DE Immunostimulatory nucleic acid #686.
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 XX WO200122972-A2.
 PN
 XX
 PD 05-APR-2001.
 XX
 XX 25-SEP-2000; 2000WO-US026383.
 PF
 XX 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 XX Krieg AM, Schetter C, Vollmer J;
 PI
 XX
 XX WPI; 2001-273485/28.
 DR
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 XX Claim 101; Page 53; 338pp; English.
 PS
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 XX Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.85e+05 Length: 28
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 4 Gaps: 0

US-09-544-776-2 (1-373) x AAF99570 (1-28)
 QY 139 ProProAlaArgProProProPro 147
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 30
 ABS78286
 ID ABS78286 standard; DNA; 28 BP.
 XX
 AC ABS78286;
 XX
 XX 13-DEC-2002 (first entry)
 DT
 XX Angiogenesis inhibitory oligonucleotide #770.
 DE
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 XX WO200253141-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX (COLE-) COLEY PHARM GROUP INC.
 PA
 XX Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 33; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, and
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 XX Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.85e+05 Length: 28
 Score: 46.00 Matches: 7
 Percent Similarity: 77.8% Conservative: 0
 Best Local Similarity: 77.8% Mismatches: 2
 Query Match: 2.4% Indels: 0
 DB: 6 Gaps: 0

US-09-544-776-2 (1-373) x ABS78286 (1-28)

QY 139 ProProAlaArgProProProPro 147
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 31
 ABL38794
 ID ABL38794 standard; DNA; 28 BP.
 XX
 AC ABL38794;
 XX
 XX 16-APR-2002 (first entry)
 DT
 XX Immunostimulatory nucleic acid SEQ ID NO: 171.
 DE

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 KW

OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..28
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX

PN WO200197843-A2.

XX

PD 27-DEC-2001.

XX

XX 22-JUN-2001; 2001WO-US020154.

PF

XX 22-JUN-2000; 2000US-0213346P.

XX

XX (IOWA) UNIV IOWA RES FOUND.

PA

XX Weiner G, Hartmann G;

PI WPI; 2002-154611/20.

XX

XX Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

XX

PS Disclosure; Page 139; 312pp; English.

XX

XX The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx

CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the

CC exemplification of the invention

XX

SQ Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 6 Gaps: 0
US-09-544-776-2 (1-373) x ABL38794 (1-28)
QY 139 ProProAlaArgProProProPro 147
ID ACH03108 standard; DNA; 28 BP.
XX ACH03108;
AC ACH03108;
XX 25-SEP-2003 (first entry)
DT Immunostimulatory nucleic acid #743.
DE Immunostimulatory nucleic acid #743.
XX Immunostimulatory; antiinflammatory; dermatological, antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX Synthetic.
OS US2003050268-A1.
XX 13-MAR-2003.
PD 29-MAR-2002; 2002US-00112653.
XX 29-MAR-2001; 2001US-0279642P.
XX (KRIE/) KRIEG A. M.
XX (BERG/) BERG D. J.
XX Krieg AM, Berg DJ;
XX WPI; 2003-521815/49.
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX disease by administering an immunostimulatory nucleic acid.
XX Disclosure; Page 29; 229pp; English.
XX The invention describes a method of treating non-allergic inflammatory
XX disease comprising administering to a subject having or at risk of
XX developing a non-allergic inflammatory disease an immunostimulatory
XX nucleic acid for prevention or treatment of the disease. The method is
XX useful for treating non-allergic inflammatory diseases, such as
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX This sequence represents an immunostimulatory nucleic acid
XX Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 9 Gaps: 0
US-09-544-776-2 (1-373) x ACH03108 (1-28)
QY 139 ProProAlaArgProProProPro 147
ID ACH03108 standard; DNA; 28 BP.
XX ACH03108;
AC ACH03108;
XX 04-DEC-2003 (first entry)
DT Immunostimulatory nucleic acid #686.
DE Immunostimulatory nucleic acid #686.
XX Immunostimulatory; antiinflammatory; dermatological, antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 XX Bratzler RL, Petersen DM, Fouron Y;
 XX WPI; 2003-657977/62.
 XX
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 XX Disclosure; Page 16; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;
 Alignment Scores: Length: 28
 Pred. No.: 2.85e+05 Matches: 7
 Score: 46.00 Conservative: 0
 Percent Similarity: 77.8% Mismatches: 2
 Best Local Similarity: 77.8% Indels: 0
 Query Match: 2.4% Gaps: 0
 DB: 9
 US-09-544-776-2 (1-373) x ADB37072 (1-28)
 QY 139 ProProAlaArgProProProPro 147
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27
 RESULT 34
 ADF82756
 ID ADF82756 standard; DNA; 28 BP.
 XX
 AC ADF82756;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 DE Antiviral phosphorothioate oligonucleotide.
 XX
 KW Anti-HIV; virucide; antiviral; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..28
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate nucleotides"
 XX
 PN WO2003097661-A2.
 XX
 PD 27-NOV-2003.
 XX
 XX 16-APR-2003; 2003WO-US011593.
 XX
 PR 13-MAY-2002; 2002US-00144360.
 XX
 XX (SALU-) SALUS THERAPEUTICS.
 PA
 XX Chen Z, Ruffner D, Kohn R, Patel D;
 PI
 XX WPI; 2004-012521/01.
 DR
 XX New pharmaceutical composition comprising an oligonucleotide having a
 PT phosphorothioate inter-sugar linkage, useful for inhibiting the
 PT replication of a retrovirus, particularly HIV-1 or HIV-2.
 PT

XX Example 1; SEQ ID NO 3; 38pp; English.
 XX
 CC The present invention relates to antiviral phosphorothioate
 CC oligonucleotides that are used in claimed methods of inhibiting the
 CC replication of a retrovirus, particularly HIV-1 or HIV-2. The antiviral
 CC phosphorothioate oligonucleotides have a chain length of 32-50
 CC nucleotides, and may comprise a 3' inverted thymine base. The present
 CC sequence is that of a homopolydeoxycytidine of 28-nucleotide chain
 CC length. This was used in an example from the invention to determine the
 CC optimal nucleotide chain length. Anti-HIV effect was shown to increase in
 CC a length-dependent manner, with maximal or total inhibition achieved with
 CC phosphorothioate oligonucleotides of 36-40 nucleotides.
 XX
 SQ Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;
 Alignment Scores: Length: 28
 Pred. No.: 2.85e+05 Matches: 7
 Score: 46.00 Conservative: 0
 Percent Similarity: 77.8% Mismatches: 2
 Best Local Similarity: 77.8% Indels: 0
 Query Match: 2.4% Gaps: 0
 DB: 12
 US-09-544-776-2 (1-373) x ADF82756 (1-28)
 QY 139 ProProAlaArgProProProPro 147
 Db 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27
 RESULT 35
 ADU90086
 ID ADU90086 standard; DNA; 28 BP.
 XX
 AC ADU90086;
 XX
 XX 10-FEB-2005 (first entry)
 DT
 DE Allergic response suppressor oligonucleotide #770.
 XX
 KW ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
 KW antibacterial; virucide; immunoglobulin E antagonist; allergy;
 KW immunostimulant; asthma; rhinitis; urticaria; dermatitis;
 KW bacterial infection; viral infection.
 XX
 OS Synthetic.
 XX
 PN US2004235774-A1.
 XX
 PD 25-NOV-2004.
 XX
 PF 23-APR-2004; 2004US-00831778.
 XX
 XX 03-FEB-2000; 2000US-0179991P.
 PR
 PR 02-FEB-2001; 2001US-00776479.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 XX Bratzler RL, Petersen DM, Fouron Y;
 PI
 XX WPI; 2004-833006/82.
 DR
 XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic
 PT dermatitis, in a subject, comprises administering a first and second dose
 PT of an immunostimulatory nucleic acid.
 XX
 XX Disclosure; SEQ ID NO 770; 235pp; English.
 PS
 XX The invention relates to a method of suppressing a symptom of an allergic
 CC response in a subject by administering a first and second dose of an
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence

CC comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other CC medicaments. They can also be used in preventing bacterial and viral CC infections. This sequence represents an oligonucleotide used in the CC method of the invention.

XX
SQ Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 13 Gaps: 0

US-09-544-776-2 (1-373) x ADU90086 (1-28)

QY 139 ProProAlaArgProProProPro 147
DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 36

AED75539

ID AED75539 standard; DNA; 28 BP.

XX

AC AED75539;

XX

DT 12-JAN-2006 (first entry)

XX

DE Immunostimulatory oligonucleotide, SEQ ID 743.

XX

XX Immunostimulant; Antinflammatory; Antipsoriatic; Gastrointestinal-Gen.;
KW Antiulcer; Dermatological; Antiallergic; helper T-lymphocyte;
KW immune stimulation; inflammation; psoriasis; inflammatory bowel disease;
KW Crohns disease; ulcerative colitis; eczema; skin allergy;
KW contact dermatitis; ss; phosphorothioate.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..28

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

US2005250726-A1.

PN

PD 10-NOV-2005.

XX

PF 12-MAY-2005; 2005US-00127654.

XX

XX 29-MAR-2001; 2001US-0279642P.

PR 29-MAR-2002; 2002US-00112653.

XX

XX (IOWA) UNIV IOWA RES FOUND.

PA

XX Krieg AM, Berg DJ;

PI

XX WPI; 2005-768014/78.

DR

XX Use of an immunostimulatory nucleic acid and a cyclooxygenase inhibitor to augment T-helper cells like immune activation and to treat non-allergic inflammatory diseases, e.g. psoriasis and Crohn's disease.

PT

XX Disclosure; SEQ ID NO 743; 58pp; English.

PS

XX The present invention relates to a method for augmenting T-helper 1 cells

CC (Th1)-like immune activation in a subject. The method comprises Th1-like

CC administering an immunostimulatory nucleic acid (I) to induce Th1-like

CC immune activation; and administering a cyclooxygenase inhibitor (II) to
CC inhibit prostaglandin expression, is new. The present sequence is one
CC such immunostimulatory nucleic acid. (I) is useful for treating non-
CC allergic inflammatory diseases such as psoriasis, inflammatory bowel
CC diseases (Crohn's disease and ulcerative colitis), eczema, allergic
CC contact dermatitis or latex dermatitis.

XX
SQ Sequence 28 BP; 0 A; 28 C; 0 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e+05 Length: 28
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 14 Gaps: 0

US-09-544-776-2 (1-373) x AED75539 (1-28)

QY 139 ProProAlaArgProProProPro 147
DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 27

RESULT 37

AAC63576/c

ID AAC63576 standard; DNA; 29 BP.

XX

AC AAC63576;

XX

DT 08-FEB-2001 (first entry)

XX

DE Guanosine rich oligonucleotide GRO29-3.

XX

XX Guanosine rich oligonucleotide; GRO; antiproliferative; cytostatic;
KW antipsoriatic; tumour; breast cancer; prostate cancer; cervical cancer;
KW psoriasis; ss.

XX

OS Unidentified.

XX

PN WO200061597-A1.

XX

PD 19-OCT-2000.

XX

PF 07-APR-2000; 2000WO-US009311.

XX

PR 08-APR-1999; 99US-0128316P.

PR 19-AUG-1999; 99US-0149823P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Miller DM, Bates PJ, Trent JO;

XX

XX WPI; 2000-679459/66.

XX

PT Use of guanosine rich oligonucleotides capable of binding to nucleolin and/or nucleolin-like cellular proteins for inhibiting growth and proliferation of neoplastic, dysplastic or hyperproliferative cells.

PT

XX Claim 18; Page 13; 78pp; English.

PS

XX The present invention relates to a method for inhibiting the

CC proliferation of malignant, dysplastic and/or hyperproliferative cells in
CC a subject, which comprises administering a guanosine rich oligonucleotide
CC (GRO). The present sequence is one such GRO. The present sequence is

CC useful for inhibiting the growth of tumour cells and for inhibiting the
CC proliferation of malignant dysplastic and/or hyperproliferative cells
CC for the treatment of conditions such as cancer e.g. breast cancer,

CC prostate cancer or cervical cancer, or psoriasis

XX

SQ Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.94e+05 Length: 29

Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x AAC63576 (1-29)

Qy 139 ProProAlaArgProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 38

AAD64858/C

ID AAD64858 standard; DNA; 29 BP.

XX

AC AAD64858;

XX

DT 11-MAR-2004 (first entry)

XX

DE Non-antisense oligonucleotide, GRO29-3.

XX

KW Neoplastic; malignancy; lung carcinoma; ss.

XX

OS Unidentified.

XX

PN US2003194754-A1.

XX

PD 16-OCT-2003.

XX

PF 08-APR-2002; 2002US-00118854.

XX

PR 08-APR-2002; 2002US-00118854.

XX

PA (MILL/) MILLER D M.

XX

PA (BATE/) BATES P J.

XX

PA (TREN/) TRENT J O.

XX

PA (XUX/) XU X.

XX

PI Miller DM, Bates PJ, Trent JO, Xu X;

XX

DR WPI; 2003-875400/81.

XX

XX Determining neoplastic state of cell, involves detecting presence of

PT plasma membrane nucleotide in cell or quantifying amount of plasma

PT membrane nucleolin in cell.

XX

XX Claim 11; SEQ ID NO 3; Opp; English.

PS

XX The present invention relates to method for determining neoplastic state

CC of a cell, involves detecting the presence of plasma membrane nucleotide

CC in the cell or quantifying the amount of plasma membrane nucleolin in the

CC cell. The invention is useful for diagnosing pre-malignant cells,

CC malignant cells and lung small cell carcinoma. The present sequence is a

CC non-antisense oligonucleotide

XX

SQ Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 2.94e+05 Length: 29

Score: 46.00 Matches: 7

Percent Similarity: 77.8% Conservative: 0

Best Local Similarity: 77.8% Mismatches: 2

Query Match: 2.4% Indels: 0

DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x AAD64858 (1-29)

Qy 139 ProProAlaArgProProProPro 147

Db 29 CCACCACCACCACCACCACCACCACCA 3

Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x AAC63576 (1-29)

Qy 139 ProProAlaArgProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 38

AAD64858/C

ID AAD64858 standard; DNA; 29 BP.

XX

AC AAD64858;

XX

DT 11-MAR-2004 (first entry)

XX

DE Non-antisense oligonucleotide, GRO29-3.

XX

KW Neoplastic; malignancy; lung carcinoma; ss.

XX

OS Unidentified.

XX

PN US2003194754-A1.

XX

PD 16-OCT-2003.

XX

PF 08-APR-2002; 2002US-00118854.

XX

PR 08-APR-2002; 2002US-00118854.

XX

PA (MILL/) MILLER D M.

XX

PA (BATE/) BATES P J.

XX

PA (TREN/) TRENT J O.

XX

PA (XUX/) XU X.

XX

PI Miller DM, Bates PJ, Trent JO, Xu X;

XX

DR WPI; 2003-875400/81.

XX

XX Determining neoplastic state of cell, involves detecting presence of

PT plasma membrane nucleotide in cell or quantifying amount of plasma

PT membrane nucleolin in cell.

XX

XX Claim 11; SEQ ID NO 3; Opp; English.

PS

XX The present invention relates to method for determining neoplastic state

CC of a cell, involves detecting the presence of plasma membrane nucleotide

CC in the cell or quantifying the amount of plasma membrane nucleolin in the

CC cell. The invention is useful for diagnosing pre-malignant cells,

CC malignant cells and lung small cell carcinoma. The present sequence is a

CC non-antisense oligonucleotide

XX

SQ Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 2.94e+05 Length: 29

Score: 46.00 Matches: 7

Percent Similarity: 77.8% Conservative: 0

Best Local Similarity: 77.8% Mismatches: 2

Query Match: 2.4% Indels: 0

DB: 10 Gaps: 0

US-09-544-776-2 (1-373) x AAD64858 (1-29)

Qy 139 ProProAlaArgProProProPro 147

Db 29 CCACCACCACCACCACCACCACCACCA 3

ADI28707/c

ID ADI28707 standard; DNA; 29 BP.

XX

AC ADI28707;

XX

DT 22-APR-2004 (first entry)

XX

DE Guanosine-rich oligonucleotide GRO29-3, used in apoptosis detection.

XX

KW Apoptosis; nucleolin; AIDS; cancer; neurodegenerative disease;

XX autoimmune disease; infection; diagnosis; ss.

OS Synthetic.

XX

PN WO2004003554-A1.

XX

PD 08-JAN-2004.

XX

PF 26-JUN-2003; 2003WO-US020167.

XX

PR 26-JUN-2002; 2002US-0392143P.

XX

PA (UYLO-) UNIV LOUISVILLE RES.FOUND INC.

XX

PA (BATE/) BATES P J.

XX

PA (MIYY/) MI Y.

XX

PI Bates PJ, Mi Y;

XX

DR WPI; 2004-083166/08.

XX

XX Detecting apoptosis comprises preparing a sample from which cells have

PT been removed and detecting at least one of nucleolin and PARP-I in the

PT sample.

XX

XX Claim 8; SEQ ID NO 2; 66pp; English.

XX

The present sequence is that of a guanosine-rich oligonucleotide (GRO), denoted GRO29-3, that can be used in the method of the invention. The method is for the detection of apoptosis. It involves preparing a sample from which cells have been removed, and detecting nucleolin and/or poly(ADP-ribose) polymerase (PARP-I) in the sample, where the sample is blood, serum, plasma, tissue, tissue culture medium or sputum. Detection of nucleolin involves detection of a complex between nucleolin and a nucleolin binding molecule, preferably an anti-nucleolin antibody or a GRO, such as the present GRO. The method allows detection of excessive apoptosis in a subject suspected of having AIDS, a neurodegenerative disease, an ischaemic injury, an autoimmune disease, a tumour, a cancer (especially endocervical adenocarcinoma, prostatic carcinoma, breast cancer, leukaemia and non-small cell lung carcinoma), a viral infection, an acute inflammatory condition or sepsis (all claimed).

XX

SQ Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 2.94e+05 Length: 29

Score: 46.00 Matches: 7

Percent Similarity: 77.8% Conservative: 0

Best Local Similarity: 77.8% Mismatches: 2

Query Match: 2.4% Indels: 0

DB: 12 Gaps: 0

US-09-544-776-2 (1-373) x ADI28707 (1-29)

Qy 139 ProProAlaArgProProProPro 147

Db 29 CCACCACCACCACCACCACCACCACCA 3

RESULT 40

ADY53899/c

ID ADY53899 standard; DNA; 29 BP.

XX

AC ADY53899;

XX

DT 19-MAY-2005 (first entry)
XX
DE Non-antisense GRO nucleolin-binding oligonucleotide GRO29A.
XX
KW Diagnosis; therapy; tumor; cancer; neoplasm; cytostatic; nucleolin; ss;
KW guanine-rich oligonucleotide; gene silencing; RNA interference; melanoma;
KW lymphoma; sarcoma; glioma; leukemia; hepatocellular carcinoma.
XX
OS Synthetic.
XX
XX US2005053607-A1.
XX
XX 10-MAR-2005.
XX
XX 09-OCT-2003; 2003US-00683480.
XX
XX 08-APR-2002; 2002US-00118854.
XX
XX (BATE/) BATES P J.
XX (MILL/) MILLER D M.
XX (TREN/) TRENT J O.
XX (XUX/) XU X.
XX
XX Bates PJ, Miller DM, Trent JO, Xu X;
XX
XX WPI; 2005-213006/22.
XX
XX Treating cancer in a subject comprises administering to the subject a
XX therapeutically effective amount of an anti-nucleolin agent and a
XX carrier.
XX
XX Disclosure; SEQ ID NO 3; 32pp; English.
XX
XX The invention relates to treating cancer in a subject comprises
XX administering to the subject a therapeutically effective amount of an
XX anti-nucleolin agent and a carrier. Also included is a pharmaceutical
XX composition comprising a nucleolin antibody or an inhibitory RNA against
XX nucleolin, and a carrier. The method and antibodies, RNA and composition
XX are useful for treating cancer, such as melanoma, lymphoma, plasmocytoma,
XX sarcoma, glioma, thymoma, leukemia, hepatoma, or breast, prostate, colon,
XX liver, esophageal, brain, lung, ovary or cervical cancer. The present
XX sequence is a GRO (guanine-rich oligonucleotide) which binds to nucleolin
XX (thereby inhibiting cancer cell growth).
XX
XX Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2.94e+05 Length: 29
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 14 Gaps: 0
US-09-544-776-2 (1-373) x ADY53899 (1-29)
QY 139 ProProAlaArgProProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3
RESULT 41
ADZ58621/C
ID ADZ58621 standard; DNA; 29 BP.
XX
XX ADZ58621;
AC
XX 14-JUL-2005 (first entry)
DT
DE Inflammation treatment-related GRO 29-3 oligonucleotide SeqID3.
XX
XX inflammation; antiinflammatory; analgesic; gynecological; hepatotropic;
KW neuroprotective; nontropic; antiarthritic; antirheumatic;
KW gastrointestinal-Gen.; antiulcer; gene therapy; dysmenorrhea;

KW alcoholic hepatitis; pancreatitis; Alzheimers disease;
KW rheumatoid arthritis; asthma; gastrointestinal disease; psoriasis;
KW atherosclerosis; Crohns disease; ulcerative colitis; GRO 29-3; ss.
XX
OS Unidentified.
XX
XX WO2005037323-A2.
PN
XX
XX 28-APR-2005.
PD
XX
XX 08-OCT-2004; 2004WO-US033185.
PF
XX
XX 10-OCT-2003; 2003US-0510466P.
PR
XX
XX (UYLO-) UNIV LOUISVILLE RES FOUND INC.
PA
XX
XX Bates PJ, Girvan AC, Barve SS;
PI
XX
XX WPI; 2005-315628/32.
DR
XX
XX Treating inflammation, e.g. acute or chronic inflammation such as
XX rheumatoid arthritis, asthma, psoriasis, and atherosclerosis, in a
XX patient comprises administering to the patient a composition comprising a
XX GRO.
XX
XX Disclosure; SEQ ID NO 3; 60pp; English.
XX
XX This invention relates to a novel method for treating inflammation in a
XX patient which comprises administering to the patient a composition
XX comprising a GRO (guanosine-rich oligonucleotide). The invention may be
XX useful for the development of compounds with an antiinflammatory,
XX analgesic, gynecological, hepatotropic, neuroprotective, nontropic,
XX antiarthritic, antirheumatic, gastrointestinal-Gen. or antiulcer activity
XX whilst the disclosed sequence may prove useful for gene therapy. The
XX methods are useful for treating inflammation associated with an acute
XX inflammatory condition. The acute inflammatory condition is selected from
XX primary dysmenorrhea, acute alcoholic liver disease and acute
XX pancreatitis. The inflammation may also be of Alzheimer's disease or
XX associated with a chronic inflammatory disease. The chronic inflammatory
XX disease is selected from rheumatoid arthritis, asthma, gastrointestinal
XX tract disease, psoriasis, atherosclerosis, Crohns disease, ulcerative
XX colitis alcohol, chronic alcoholic liver disease, non-alcoholic
XX steatohepatitis and chronic pancreatitis. The present sequence is that of
XX the oligonucleotide GRO 29-3 which was used during the development of the
XX novel method of the invention.
XX
XX Sequence 29 BP; 0 A; 0 C; 18 G; 11 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2.94e+05 Length: 29
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 14 Gaps: 0
US-09-544-776-2 (1-373) x ADZ58621 (1-29)
QY 139 ProProAlaArgProProProProPro 147
Db 29 CCACCACCACCACCACCACCACCACCA 3
RESULT 42
AAQ20873
ID AAQ20873 standard; DNA; 30 BP.
XX
XX AAQ20873;
AC
XX 11-MAY-1992 (first entry)
DT
DE Immunostimulatory oligonucleotide #28 contg. palindrome.
XX natural killer cell; NK; immunodeficiency; autoimmune disease; CSF;
KW

PF 24-JUN-1994; 94WO-US007234.
XX
PR 25-JUN-1993; 93US-00083088.
XX
XX (UYVA) UNIV YALE.
PA
PI Glazer PM, Havre PA;
XX
XX WPI; 1995-060943/08.
DR
XX
XX New mutagenic oligo:nucleotide(s) - having a mutagen incorporated in an
PT oligo:nucleotide which forms a triplex, for site-directed mutagenesis.
PT
XX
XX Example 5; Fig 6; 72pp; English.
PS
XX AAQ81071 is the supF gene triplex forming mutagenic oligonucleotide pso-
CC AGT30. It forms a triplex (a triple stranded nucleic acid) with a
CC specific site on the supF genome, enabling the covalently bound
CC 4'hydroxymethyl-4,5',8-trimethylpsoralen group to produce a site specific
CC mutation. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 30 BP; 5 A; 0 C; 23 G; 2 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 3.03e+05 Length: 30
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AAQ81071 (1-30)

QY 139 ProProAlaArgProProProProProProAla 149
ID AAT70013 standard; DNA; 30 BP.
DB 28 CCCCCT-----CCCCCACCACCCCTTCC 2

RESULT 45
AAT70013/C
ID AAT70013 standard; DNA; 30 BP.
XX
XX
AC AAT70013;
XX
XX 25-AUG-1997 (first entry)
XX
XX Triplex-forming oligonucleotide AGT30.
XX
XX Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;
KW oncogene inactivation; supF gene; ss.
XX
XX Synthetic.
XX
XX WO9639195-A2.
PN
XX
XX 12-DEC-1996.
PD
XX
XX 04-JUN-1996; 96WO-US008883.
PF
XX
XX 06-JUN-1995; 95US-00463519.
PR
XX
XX (UYVA) UNIV YALE.
PA
XX
XX Glazer PM, Havre PA;
PI
XX
XX WPI; 1997-042873/04.
DR
XX
XX Triple-helix forming oligo:nucleotide linked to a mutagen - useful for
PT site-specific mutagenesis of target gene, e.g. for gene therapy or to
PT inactivate oncogene(s) or viral genes.
XX
XX Example 5; Page 33; 68pp; English.
PS
XX
XX Oligonucleotide AGT30 (AAT70013) was designed to form a triple helix at a

CC 30-bp polypurine/polypyrimidine site in supFG1a (AAT70015), a modified
CC supF gene (see also AAT70005). It was used to test intracellular
CC targeted mutagenesis via triplex formation, using an SV40 vector in vivo
CC in monkey COS cells. Administration of psoralen-linked AGT30 followed
CC after 2 hr by UVA irradiation induced mutations in 2.1% of the vector
CC molecules. There was a high specificity for T:A to A:T transversions at
CC the predicted psoralen intercalation site (bp 166 of supF)
XX
XX Sequence 30 BP; 5 A; 0 C; 23 G; 2 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 3.03e+05 Length: 30
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AAT70013 (1-30)

QY 139 ProProAlaArgProProProProProProAla 149
ID AAT70013 standard; DNA; 30 BP.
DB 28 CCCCCT-----CCCCCACCACCCCTTCC 2

RESULT 46
AAT7060/C
ID AAT7060 standard; DNA; 30 BP.
XX
XX
AC AAT7060;
XX
XX 05-SEP-1997 (first entry)
XX
XX Oligonucleotide AG30, which binds triplex target site in supFG1.
DE
XX
XX Triplex; supFG1; forming; target site; triple stranded; induction;
KW mutation; targetted mutagenesis; triple helix; ss.
XX
XX Synthetic.
XX
XX WO9640898-A1.
PN
XX
XX 19-DEC-1996.
PD
XX
XX 03-JUN-1996; 96WO-US008392.
PF
XX
XX 07-JUN-1995; 95US-00476712.
PR
XX
XX (UYVA) UNIV YALE.
PA
XX
XX Glazer PM;
PI
XX
XX WPI; 1997-052310/05.
DR
XX
XX Oligo-nucleotide for targetted mutagenesis of double stranded nucleic
PT acid mol. - by forming triple stranded nucleic acid mol. with target
PT region of double stranded nucleic acid mol.
XX
XX
XX Example 1; Fig 1; 29pp; English.
XX
XX In an example of the invention, the binding of the oligonucleotides AG10
CC (AAT7062), AG20 (AAT7061) and AG30 (AAT7060) to the supFG1 triplex
CC target site (AAT7059), was examined using a gel mobility shift assay.
CC Based on the concentration dependence of the triplex formation, the
CC equilibrium constants for AG10, AG20 and AG30 were 3x10 power -5, 3x10
CC power -7 and 2x10 power -8. The oligonucleotides were then tested for
CC their ability to induce mutations in the pSupFG1 SV40 vector in monkey
CC COS cells. AG30 generated mutations in the target gene at a frequency of
CC 0.2%, 13 fold over the spontaneous background in the assay. In contrast,
CC AG10 and AG20, which show inferior 3rd strand binding to supFG1, were
CC much less effective in producing mutations. Examples of some of the
CC mutations induced in the pSupFG1 vector using the oligonucleotides are
CC given in AAT75067-73
XX

SQ Sequence 30 BP; 5 A; 0 C; 23 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.03e+05 Length: 30
Score: 46.00 Matches: 8
Percent Similarity: 81.8% Conservative: 1
Best Local Similarity: 72.7% Mismatches: 0
Query Match: 2.4% Indels: 2
DB: 2 Gaps: 1

US-09-544-776-2 (1-373) x AAT47060 (1-30)

QY 139 ProProAlaArgProProProProProAla 149
ID AAX27663 standard; DNA; 30 BP.
XX
AC AAX27663;
XX
DT 01-JUN-1999 (first entry)
XX
DE DNA encoding a HRGP motif.
XX
KW Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP;
KW repetitive proline-rich protein; RERP; arabino-galactan protein; AGP;
KW glycopeptide; ss.
XX
OS Acacia sp.
XX
PN WO9903978-A1.
XX
PD 28-JAN-1999.
XX
PF 21-JUL-1998; 98WO-US015083.
XX
PR 21-JUL-1997; 97US-00897556.
PR 20-JUL-1998; 98US-00119507.
XX
PA (UYOH-) UNIV OHIO.
XX
PI Kielaszewski MJ;
XX
DR WPI; 1999-132225/11.
XX
PT Novel synthetic gene designed from repetitive peptide sequences - of
XX hydroxyproline-rich glycoprotein.
PS Claim 1; Page 5; 72pp; English.
XX
CC The invention relates to novel synthetic genes for plant gums. A new
CC approach is described to the production of hydroxyproline-rich
CC glycoproteins (HRGPs), repetitive proline-rich proteins (RPRPs) and
CC arabino-galactan proteins (AGPs). Synthetic genes comprising a nucleic
CC acid encoding the peptide (AAY01267) can be engineered for the production
CC of repetitive glycopeptide modules in cells. The invention provided a new
CC approach to the problem of producing plant gums that is not dependent on
CC environmental factors and greatly simplifies the production of a variety
CC of naturally occurring gums as well as designer gums. Note: The present
CC nucleotide sequence is indicated as a peptide sequence in the claims
XX
SQ Sequence 30 BP; 6 A; 19 C; 0 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.03e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 70.0% Conservative: 0
Best Local Similarity: 70.0% Mismatches: 3
Query Match: 2.4% Indels: 0
DB: 2 Gaps: 0

US-09-544-776-2 (1-373) x AAX27663 (1-30)

QY 139 ProProAlaArgProProProProPro 148
ID AAX27663 standard; DNA; 30 BP.
XX
AC AAX27663;
XX
DT 06-AUG-2003 (revised)
DT 16-JUL-2002 (first entry)
XX
DE Litopenaeus vannamei microsatellite detection probe 2.
XX
KW Giant black tiger prawn; Penaeus monodon; pacific white shrimp;
KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;
KW Taura Syndrome Virus; TSV; infection; probe; ss.
XX
OS Litopenaeus vannamei.
OS Synthetic.
XX
PN WO200034476-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029571.
XX
PR 10-DEC-1998; 98US-0111670P.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Alcivar-Warren A, Xu Z, Dhar AK, Fan Y, Meehan D, Garcia DK;
XX
DR WPI; 2000-423422/36.
XX
PT Polynucleotides of shrimp are useful for identifying, mapping and
PT characterizing of the genome of various species of shrimp.
XX
PS Page 60; Example 4; 120pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) of the giant
CC black tiger prawn, Penaeus monodon or expressed sequence tags of the
CC pacific white shrimp, Litopenaeus vannamei (ABN80937-ABN81172), both
CC containing microsatellites sequences including those P. monodon
CC microsatellite sequences given in GenBank AF077550-AF077598. (I), the
CC complementary sequence or fragment and the encoded polypeptide are useful
CC for mapping of the genome of various species of shrimp. Mapping the
CC genome of Penaeus is useful for determining whether a test shrimp,
CC preferably Litopenaeus vannamei, has a genotype associated with a
CC phenotypic trait such as resistance to Taura Syndrome Virus (TSV)
CC infection. The present sequence is that of a probe, useful in examples of
CC the invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 30 BP; 0 A; 20 C; 0 G; 10 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.03e+05 Length: 30
Score: 46.00 Matches: 7
Percent Similarity: 77.8% Conservative: 0
Best Local Similarity: 77.8% Mismatches: 2
Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0

US-09-544-776-2 (1-373) x ABN81202 (1-30)

QY 139 ProProAlaArgProProProProPro 147
ID AAX27663 standard; DNA; 30 BP.
XX
AC AAX27663;
XX
DT 06-AUG-2003 (revised)
DT 16-JUL-2002 (first entry)
XX
DE Litopenaeus vannamei microsatellite detection probe 2.
XX
KW Giant black tiger prawn; Penaeus monodon; pacific white shrimp;
KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;
KW Taura Syndrome Virus; TSV; infection; probe; ss.
XX
OS Litopenaeus vannamei.
OS Synthetic.
XX
PN WO200034476-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029571.
XX
PR 10-DEC-1998; 98US-0111670P.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Alcivar-Warren A, Xu Z, Dhar AK, Fan Y, Meehan D, Garcia DK;
XX
DR WPI; 2000-423422/36.
XX
PT Polynucleotides of shrimp are useful for identifying, mapping and
PT characterizing of the genome of various species of shrimp.
XX
PS Page 60; Example 4; 120pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) of the giant
CC black tiger prawn, Penaeus monodon or expressed sequence tags of the
CC pacific white shrimp, Litopenaeus vannamei (ABN80937-ABN81172), both
CC containing microsatellites sequences including those P. monodon
CC microsatellite sequences given in GenBank AF077550-AF077598. (I), the
CC complementary sequence or fragment and the encoded polypeptide are useful
CC for mapping of the genome of various species of shrimp. Mapping the
CC genome of Penaeus is useful for determining whether a test shrimp,
CC preferably Litopenaeus vannamei, has a genotype associated with a
CC phenotypic trait such as resistance to Taura Syndrome Virus (TSV)
CC infection. The present sequence is that of a probe, useful in examples of
CC the invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 30 BP; 0 A; 20 C; 0 G; 10 T; 0 U; 0 Other;

RESULT 49

AAA05780
ID AAA05780 standard; DNA; 30 BP.
AC
XX
AA05780;
XX
DT 05-JUN-2000 (first entry)
XX
DE Streptavidin display linker DNA, SEQ ID NO:234.
XX
KW Phage display; bacteriophage M13; fusion protein; major coat protein;
KW protein VIII; phagemid vector; electroporation; combinatorial library;
KW streptavidin; SAV; ss.
XX
OS Synthetic.
XX
PN WO200006717-A2.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US016596.
XX
PR 27-JUL-1998; 98US-0094291P.
PR 08-OCT-1998; 98US-0103514P.
PR 10-MAY-1999; 98US-013296P.
PR 19-MAY-1999; 99US-0134870P.
XX
PA (GETH) GENENTECH INC.
XX
PI Sidhu SS, Weiss GA, Wells JA;
XX
DR WPI; 2000-183122/16.
DR P-PSDB; AAY81337.
XX
PT Fusion proteins comprising a heterologous protein and a viral variant
PT major coat protein useful in phage display systems for improving
PT transformation efficiency.
XX
PS Disclosure; Fig 7B; 118pp; English.
XX
CC The invention relates to novel fusion proteins comprising a heterologous
CC polypeptide fused to a variant (non-wild type) bacteriophage major coat
CC protein (protein VIII). The invention also relates to replicable
CC expression vectors which contain a gene encoding the fusion protein; host
CC cells containing the expression vectors; phages which display the fusion
CC protein on their surface; phage libraries displaying a plurality of
CC different fusion proteins on viral surfaces; and methods of using these
CC compositions. The fusion proteins the invention are well tolerated in
CC phage display systems. Variants of the major coat proteins can be used to
CC alter the number of fusion proteins incorporated into a virus particle.
CC Hyper-functional variants can be used to increase the number of fusion
CC proteins incorporated into a virus particle. Conversely, hypo-functional
CC variants can be used to decrease fusion protein incorporation. This is
CC useful for tailoring the incorporation of fusion proteins into virus
CC particles to achieve a desired level of valency. The variant replicable
CC plasmid/phagemid vectors are useful for producing polypeptides of
CC interest. The methods are useful for improving the transformation of
CC cells by highly purifying DNA. The present invention uses affinity DNA
CC purification to reduce ionic impurities and thus reduce the conductance
CC associated with a unit mass of DNA. This is an advantageous in
CC electroporation methods for increasing the concentration of DNA present.
CC The increase in DNA entering the host cell provides a greater number of
CC transformants per electroporation and allows one to prepare larger
CC combinatorial libraries which overcomes the prior art problem of small
CC library size using recombinant DNA. Sequences AAA05768-A05795 represent
CC DNA encoding linkers selected for display of streptavidin (SAV)
XX
SQ Sequence 30 BP; 6 A; 22 C; 2 G; 0 T; 0 U; 0 Other;
XX
Alignment Scores: 3.03e+05 Length: 30
Pred. No.: 46.00 Matches: 7
Score: 87.5% Conservative: 0
Percent Similarity: 87.5% Mismatches: 1
Best Local Similarity: 87.5%

Query Match: 2.4% Indels: 0
DB: 3 Gaps: 0
US-09-544-776-2 (1-373) x AAA05780 (1-30)
Qv 140 ProAlaArgProProProProPro 147
||| ||||| ||||| ||||| |||||
Db 3 CCCCCAGCACCACCCACCCGCCCA 26
RESULT 50
AAI65861/c
ID AAI65861 standard; DNA; 30 BP.
XX
AC AAI65861;
XX
DT 03-JAN-2002 (first entry)
XX
DE Nucleotide sequence of triplex forming oligonucleotide for Hprt gene.
XX
KW DNA-modifying molecule; DNA repair-deficient cell; transgenic cell;
KW disease model; Hprt gene; triplex forming oligonucleotide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /tag= a
FT /note= "psoralen attached"
XX
PN WO200173001-A2.
XX
PD 04-OCT-2001.
XX
PF 22-MAR-2001; 2001WO-US009218.
XX
PR 24-MAR-2000; 2000US-0191996P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Seidman MM, Majumdar A;
XX
DR WPI; 2001-616491/71.
XX
PT Modifying nucleotide sequence, including recombination of genes in (non-
PT)human cell, comprises introducing DNA-modifying molecule into cell cycle
PT synchronized cell.
XX
PS Example 4; Page 49; 67pp; English.
XX
CC The specification describes a method for modifying a nucleotide sequence
CC in the genome of a cell. The method comprises providing a cell and a DNA-
CC modifying molecule, manipulating the cell to generate a synchronized cell
CC and contacting the synchronized cell with the DNA-modifying molecule
CC under conditions such that a modification in the nucleotide sequence is
CC produced. The method is useful for modifying nucleotide sequences in the
CC genome of a human or non-human cell including a fertilized egg cell from
CC an animal such as sheep, pig, rabbit, cattle and a mouse cell such as
CC blastomere, eight-cell embryo cell, blastocoele, midgestation embryo cell
CC and embryonic stem cell. The cell is preferably DNA repair-deficient. The
CC method is useful for introducing a modification into the genome of a cell
CC for determining the effect of the modification on the cell. The method
CC generates transgenic cells and animals useful as models for diseases, and
CC for screening therapeutic agents. The method also facilitates targeted
CC recombination for producing gene knockout organisms and/or replacement of
CC defective genes with non-defective genes. Further the method is useful
CC for determining the function of a gene of unknown function. AAI65861-62
CC represent triplex forming oligonucleotides, which were used in the method
CC of the invention to modify a fragment of the Hprt gene
XX
SQ Sequence 30 BP; 5 A; 0 C; 23 G; 2 T; 0 U; 0 Other;
XX
Alignment Scores: 3.03e+05 Length: 30
Pred. No.: 30

Score:	46.00	Matches:	8
Percent Similarity:	81.8%	Conservative:	1
Best Local Similarity:	72.7%	Mismatches:	0
Query Match:	2.4%	Indels:	2
DB:	4	Gaps:	1

US-09-544-776-2 (1-373) x AAI65861 (1-30)

Qy 139 ProProAlaArgProProProProProProAla 149

Db
28 CCCCCT-----CCCCACACCCCCCCCCCTTC 2

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Job time : 787 secs

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